

#9



SEQUENCE LISTING

1) GENERAL INFORMATION:

(i) APPLICANT: BROW, MARY ANN D.
LYAMICHEV, VICTOR I.
OLIVE, DAVID M.

(ii) TITLE OF INVENTION: RAPID DETECTION AND IDENTIFICATION OF
PATHOGENS

(iii) NUMBER OF SEQUENCES: 165

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MEDLEN & CARROLL
(B) STREET: 220 MONTGOMERY STREET, SUITE 2200
(C) CITY: SAN FRANCISCO
(D) STATE: CALIFORNIA
(E) COUNTRY: UNITED STATES OF AMERICA
(F) ZIP: 94104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: CARROLL, PETER G.
(B) REGISTRATION NUMBER: 32,837
(C) REFERENCE/DOCKET NUMBER: FORS-01756

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 705-8410
(B) TELEFAX: (415) 397-8338

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAGGGGGA TGCTGCCCCT CTTTGAGCCC AAGGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CCACGCCCTG AAGGGCCTCA CCACCAGCCG GGGGGAGCCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTCAAGGA GGACGGGGAC	180
GCGGTGATCG TGGTCTTTGA CGCCAAGGCC CCCTCCTTCC GCCACGAGGC CTACGGGGGG	240

TACAAGGCGG	GCCGGGCCCC	CACGCCGGAG	GACTTTCCCC	GGCAACTCGC	CCTCATCAAG	300
GAGCTGGTGG	ACCTCCTGGG	GCTGGCGCGC	CTCGAGGTCC	CGGGCTACGA	GGCGGACGAC	360
GTCTTGCCCA	GCCTGGCCAA	GAAGGCGGAA	AAGGAGGGCT	ACGAGGTCCG	CATCCTCACC	420
CCCACAAAG	ACCTTTACCA	GCTCCTTTCC	GACCGCATCC	ACGTCTCTCA	CCCCGAGGGG	480
TACCTCATCA	CCCCGGCCTG	GCTTTGGGAA	AAGTACGGCC	TGAGGCCCCG	CCAGTGGGCC	540
GACTACCGGG	CCCTGACCGG	GGACGAGTCC	GACAACCTTC	CCGGGGTCAA	GGGCATCGGG	600
GAGAAGACGG	CGAGGAAGCT	TCTGGAGGAG	TGGGGGAGCC	TGGAAGCCCT	CCTCAAGAAC	660
CTGGACCGGC	TGAAGCCCGC	CATCCGGGAG	AAGATCCTGG	CCCACATGGA	CGATCTGAAG	720
CTCTCCTGGG	ACCTGGCCAA	GGTGCACACC	GACCTGCCCC	TGGAGGTGGA	CTTCGCCAAA	780
AGGCGGGAGC	CCGACCGGGA	GAGGCTTAGG	GCCTTTCTGG	AGAGGCTTGA	GTTTGGCAGC	840
CTCCTCCACG	AGTTCGGCCT	TCTGGAAAAGC	CCCAAGGCCC	TGGAGGAGGC	CCCCTGGCCC	900
CCGCCGGAAG	GGGCCTTCGT	GGGCTTTGTG	CTTTCCCGCA	AGGAGCCCAT	GTGGGCCGAT	960
CTTCTGGCCC	TGGCCGCCGC	CAGGGGGGGC	CGGGTCCACC	GGGCCCCCGA	GCCTTATAAA	1020
GCCCTCAGGG	ACCTGAAGGA	GGCGCGGGGG	CTTCTCGCCA	AAGACCTGAG	CGTTCTGGCC	1080
CTGAGGGAAG	GCCTTGCCCT	CCCGCCCGGC	GACGACCCCA	TGCTCCTCGC	CTACCTCCTG	1140
GACCTTCCA	ACACCACCCC	CGAGGGGGTG	GCCCGGCGCT	ACGGCGGGGA	GTGGACGGAG	1200
GAGGCGGGGG	AGCGGGCCGC	CCTTTCCGAG	AGGCTCTTCG	CCAACCTGTG	GGGGAGGCTT	1260
GAGGGGGAGG	AGAGGCTCCT	TTGGCTTTAC	CGGGAGGTGG	AGAGGCCCTT	TTCCGCTGTC	1320
CTGGCCCACA	TGGAGGCCAC	GGGGGTGCGC	CTGGACGTGG	CCTATCTCAG	GGCCTTGTCC	1380
CTGGAGGTGG	CCGAGGAGAT	CGCCCGCCTC	GAGGCCGAGG	TCTTCCGCCT	GGCCGGCCAC	1440
CCCTTCAACC	TCAACTCCCG	GGACCAGCTG	GAAAGGGTCC	TCTTTGACGA	GCTAGGGCTT	1500
CCCGCCATCG	GCAAGACGGA	GAAGACCGGC	AAGCGCTCCA	CCAGCGCCGC	CGTCTGGAG	1560
GCCCTCCGCG	AGGCCCACCC	CATCGTGGAG	AAGATCCTGC	AGTACCGGGA	GCTCACCAAG	1620
CTGAAGAGCA	CCTACATTGA	CCCCTTGCCG	GACCTCATCC	ACCCAGGAC	GGCCGCCTC	1680
CACACCCGCT	TCAACCAGAC	GGCCACGGCC	ACGGGCAGGC	TAAGTAGCTC	CGATCCCAAC	1740
CTCCAGAACA	TCCCCGTCCG	CACCCGCTT	GGGCAGAGGA	TCCGCCGGGC	CTTCATCGCC	1800
GAGGAGGGGT	GGCTATTGGT	GGCCCTGGAC	TATAGCCAGA	TAGAGCTCAG	GGTGCTGGCC	1860
CACCTCTCCG	GCGACGAGAA	CCTGATCCGG	GTCTTCCAGG	AGGGGCGGGA	CATCCACACG	1920
GAGACCGCCA	GCTGGATGTT	CGGCGTCCCC	CGGGAGGCCG	TGGACCCCTT	GATGCGCCGG	1980
GCGGCCAAGA	CCATCAACTT	CGGGGTCTTC	TACGGCATGT	CGGCCACCG	CCTCTCCAG	2040
GAGCTAGCCA	TCCCTTACGA	GGAGGCCCCAG	GCCTTCATTG	AGCGCTACTT	TCAGAGCTTC	2100

CCCAAGGTGC	GGGCCTGGAT	TGAGAAGACC	CTGGAGGAGG	GCAGGAGGCG	GGGGTACGTG	2160
GAGACCCTCT	TCGGCCGCCG	CCGCTACGTG	CCAGACCTAG	AGGCCCGGGT	GAAGAGCGTG	2220
CGGGAGGCGG	CCGAGCGCAT	GGCCTTCAAC	ATGCCCCGTCC	AGGGCACCGC	CGCCGACCTC	2280
ATGAAGCTGG	CTATGGTGAA	GCTCTTCCCC	AGGCTGGAGG	AAATGGGGGC	CAGGATGCTC	2340
CTTCAGGTCC	ACGACGAGCT	GGTCCTCGAG	GCCCCAAAAG	AGAGGGCGGA	GGCCGTGGCC	2400
CGGCTGGCCA	AGGAGGTCAT	GGAGGGGGTG	TATCCCCTGG	CCGTGCCCCCT	GGAGGTGGAG	2460
GTGGGGATAG	GGGAGGACTG	GCTCTCCGCC	AAGGAGTGAT	ACCACC		2506

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2496 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGGCGATGC	TTCCCCTCTT	TGAGCCCCAA	GGCCGCGTGC	TCCTGGTGGA	CGGCCACCAC	60
CTGGCCTACC	GCACCTTCTT	TGCCCTCAAG	GGCCTCACCA	CCAGCCGCGG	CGAACCCGTT	120
CAGGCGGTCT	ACGGCTTCGC	CAAAAGCCTC	CTCAAGGCCC	TGAAGGAGGA	CGGGGACGTG	180
GTGGTGGTGG	TCTTTGACGC	CAAGGCCCCC	TCCTTCCGCC	ACGAGGCCTA	CGAGGCCTAC	240
AAGGCGGGCC	GGGCCCCCAC	CCCGGAGGAC	TTTCCCCGGC	AGCTGGCCCT	CATCAAGGAG	300
TTGGTGGACC	TCCTAGGCCT	TGTGCGGCTG	GAGGTTCCTG	GCTTTGAGGC	GGACGACGTG	360
CTGGCCACCC	TGGCCAAGCG	GGCGGAAAAG	GAGGGGTACG	AGGTGCGCAT	CCTCACTGCC	420
GACCGCGACC	TCTACCAGCT	CCTTTCGGAG	CGCATCGCCA	TCCTCCACCC	TGAGGGGTAC	480
CTGATCACCC	CGGCGTGGCT	TTACGAGAAG	TACGGCCTGC	GCCCCGAGCA	GTGGGTGGAC	540
TACCGGGCCC	TGGCGGGGGA	CCCCTCGGAT	AACATCCCCG	GGGTGAAGGG	CATCGGGGAG	600
AAGACCGCCC	AGAGGCTCAT	CCGCGAGTGG	GGGAGCCTGG	AAAACCTCTT	CCAGCACCTG	660
GACCAGGTGA	AGCCCTCCTT	GCGGGAGAAG	CTCCAGGCGG	GCATGGAGGC	CCTGGCCCTT	720
TCCCGGAAGC	TTTCCCAGGT	GCACACTGAC	CTGCCCCTGG	AGGTGGACTT	CGGGAGGCGC	780
CGCACACCCA	ACCTGGAGGG	TCTGCGGGCT	TTTTTGGAGC	GGTTGGAGTT	TGGAAGCCTC	840
CTCCACGAGT	TCGGCCTCCT	GGAGGGGGCC	AAGGCGGCAG	AGGAGGCCCC	CTGGCCCCCT	900
CCGGAAGGGG	CTTTTTTGGG	CTTTTCCTTT	TCCCGTCCCG	AGCCCATGTG	GGCCGAGCTT	960
CTGGCCCTGG	CTGGGGCGTG	GGAGGGGCGC	CTCCATCGGG	CACAAGACCC	CCTTAGGGGC	1020
CTGAGGGACC	TTAAGGGGGT	GCGGGGAATC	CTGGCCAAGG	ACCTGGCGGT	TTTGGCCCTG	1080

CGGGAGGGCC TGGACCTCTT CCCAGAGGAC GACCCCATGC TCCTGGCCTA CCTTCTGGAC	1140
CCCTCCAACA CCACCCCTGA GGGGGTGGCC CGGCGTTACG GGGGGGAGTG GACGGAGGAT	1200
GCGGGGGAGA GGGCCCTCCT GGCCGAGCGC CTCTTCCAGA CCCTAAAGGA GCGCCTTAAG	1260
GGAGAAGAAC GCCTGCTTTG GCTTTACGAG GAGGTGGAGA AGCCGCTTTC CCGGGTGTGTG	1320
GCCCGGATGG AGGCCACGGG GGTCCGGCTG GACGTGGCCT ACCTCCAGGC CCTCTCCCTG	1380
GAGGTGGAGG CGGAGGTGCG CCAGCTGGAG GAGGAGGTCT TCCGCCTGGC CGGCCACCCC	1440
TTCAACCTCA ACTCCCGCGA CCAGCTGGAG CGGGTGCTCT TTGACGAGCT GGGCCTGCCT	1500
GCCATCGGCA AGACGGAGAA GACGGGGAAA CGCTCCACCA GCGCTGCCGT GCTGGAGGCC	1560
CTGCGAGAGG CCCACCCCAT CGTGGACCGC ATCCTGCAGT ACCGGGAGCT CACCAAGCTC	1620
AAGAACACCT ACATAGACCC CCTGCCCCGCC CTGGTCCACC CCAAGACCGG CCGGCTCCAC	1680
ACCCGCTTCA ACCAGACGGC CACCGCCACG GGCAGGCTTT CCAGCTCCGA CCCAACCTG	1740
CAGAACATCC CCGTGCGCAC CCCTCTGGGC CAGCGCATCC GCCGAGCCTT CGTGGCCGAG	1800
GAGGGCTGGG TGCTGGTGGT CTTGGACTAC AGCCAGATTG AGCTTCGGGT CCTGGCCAC	1860
CTCTCCGGGG ACGAGAACCT GATCCGGGTC TTTCAGGAGG GGAGGGACAT CCACACCCAG	1920
ACCGCCAGCT GGATGTTCCG CGTTTCCCCC GAAGGGGTAG ACCCTCTGAT GCGCCGGGCG	1980
GCCAAGACCA TCAACTTCGG GGTGCTCTAC GGCATGTCCG CCCACCGCCT CTCCGGGGAG	2040
CTTTCCATCC CCTACGAGGA GCGGGTGGCC TTCATTGAGC GCTACTTCCA GAGCTACCCC	2100
AAGGTGCGGG CCTGGATTGA GGGGACCCTC GAGGAGGGCC GCCGGCGGGG GTATGTGGAG	2160
ACCCTCTTCG GCCGCCGGCG CTATGTGCCC GACCTCAACG CCCGGGTGAA GAGCGTGC GC	2220
GAGGCGGCGG AGCGCATGGC CTTCAACATG CCGGTCCAGG GCACCGCCGC CGACCTCATG	2280
AAGCTGGCCA TGGTGCGGCT TTTCCCCCGG CTCAGGAAC TGGGGGCGAG GATGCTTTTG	2340
CAGGTGCACG ACGAGCTGGT CCTCGAGGCC CCAAGGACC GGGCGGAGAG GGTAGCCGCT	2400
TTGGCCAAGG AGGTCATGGA GGGGTCTGG CCCCTGCAGG TGCCCCTGGA GGTGGAGGTG	2460
GGCCTGGGGG AGGACTGGCT CTCCGCAAG GAGTAG	2496

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2504 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGGCGA	TGCTTCCGCT	CTTTGAACCC	AAAGGCCGGG	TCCTCCTGGT	GGACGGCCAC	60
CACCTGGCCT	ACCGCACCTT	CTTCGCCCTG	AAGGGCCTCA	CCACGAGCCG	GGGCGAACCG	120
GTGCAGGCGG	TCTACGGCTT	CGCCAAGAGC	CTCCTCAAGG	CCCTGAAGGA	GGACGGGTAC	180
AAGGCCGTCT	TCGTGGTCTT	TGACGCCAAG	GCCCCCTCCT	TCCGCCACGA	GGCCTACGAG	240
GCCTACAAGG	CGGGGAGGGC	CCCGACCCCC	GAGGACTTCC	CCCGGCAGCT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGTTTACC	CGCCTCGAGG	TCCCCGGCTA	CGAGGCGGAC	360
GACGTTCTCG	CCACCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAACTCGTC	TCCGACCGCG	TCGCCGTCTT	CCACCCCGAG	480
GGCCACCTCA	TCACCCCGGA	GTGGCTTTGG	GAGAAGTACG	GCCTCAGGCC	GGAGCAGTGG	540
GTGGACTTCC	GCGCCCTCGT	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCTCAA	GCTCCTCAAG	GAGTGGGGAA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTAAAGCC	AGAAAACGTC	CGGGAGAAGA	TCAAGGCCCA	CCTGGAAGAC	720
CTCAGGCTCT	CCTTGGAGCT	CTCCCGGGTG	CGCACCGACC	TCCCCCTGGA	GGTGGACCTC	780
GCCCAGGGGC	GGGAGCCCGA	CCGGGAGGGG	CTTAGGGCCT	TCCTGGAGAG	GCTGGAGTTC	840
GGCAGCCTCC	TCCACGAGTT	CGGCCTCCTG	GAGGCCCCCG	CCCCCCTGGA	GGAGGCCCCC	900
TGGCCCCCGC	CGGAAGGGGC	CTTCGTGGGC	TTCGTCTCTT	CCCGCCCCGA	GCCCATGTGG	960
GCGGAGCTTA	AAGCCCTGGC	CGCCTGCAGG	GACGGCCGGG	TGCACCGGGC	AGCAGACCCC	1020
TTGGCGGGGC	TAAAGGACCT	CAAGGAGGTC	CGGGGCCTCC	TCGCCAAGGA	CCTCGCCGTC	1080
TTGGCCTCGA	GGGAGGGGCT	AGACCTCGTG	CCCGGGGACG	ACCCCATGCT	CCTCGCCTAC	1140
CTCCTGGACC	CCTCCAACAC	CACCCCGAG	GGGGTGGCGC	GGCGCTACGG	GGGGGAGTGG	1200
ACGGAGGACG	CCGCCCACCG	GGCCCTCCTC	TCGGAGAGGC	TCCATCGGAA	CCTCCTTAAG	1260
CGCCTCGAGG	GGGAGGAGAA	GCTCCTTTGG	CTCTACCACG	AGGTGGAAAA	GCCCCCTCTC	1320
CGGGTCCTGG	CCCACATGGA	GGCCACCGGG	GTACGGCTGG	ACGTGGCCTA	CCTTCAGGCC	1380
CTTTCCCTGG	AGCTTGCGGA	GGAGATCCGC	CGCCTCGAGG	AGGAGGTCTT	CCGCTTGGCG	1440
GGCCACCCCT	TCAACCTCAA	CTCCCGGGAC	CAGCTGGAAA	GGGTGCTCTT	TGACGAGCTT	1500
AGGCTTCCCG	CCTTGGGGAA	GACGCAAAAG	ACAGGCAAGC	GCTCCACCAG	CGCCGCGGTG	1560
CTGGAGGCCC	TACGGGAGGC	CCACCCCATC	GTGGAGAAGA	TCCTCCAGCA	CCGGGAGCTC	1620
ACCAAGCTCA	AGAACACCTA	CGTGGACCCC	CTCCCAAGCC	TCGTCCACCC	GAGGACGGGC	1680
CGCCTCCACA	CCCGCTTCAA	CCAGACGGCC	ACGGCCACGG	GGAGGCTTAG	TAGCTCCGAC	1740
CCCAACCTGC	AGAACATCCC	CGTCCGCACC	CCCTTGGGCC	AGAGGATCCG	CCGGGCCTTC	1800

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GTGGCCGAGG CGGGTTGGGC GTTGGTGGCC CTGGACTATA GCCAGATAGA GCTCCGCGTC      1860
CTCGCCCACC TCTCCGGGGA CGAAAACCTG ATCAGGGTCT TCCAGGAGGG GAAGGACATC      1920
CACACCCAGA CCGCAAGCTG GATGTTTCGGC GTCCCCCGG AGGCCGTGGA CCCCTGATG      1980
CGCCGGGCGG CCAAGACGGT GAACTTCGGC GTCCTCTACG GCATGTCCGC CCATAGGCTC      2040
TCCCAGGAGC TTGCCATCCC CTACGAGGAG GCGGTGGCCT TTATAGAGGC TACTTCCAAA      2100
GCTTCCCCAA GGTGCGGGCC TGGATAGAAA AGACCTTGGA GGAGGGGAGG AAGCGGGGCT      2160
ACGTGGAAAC CCTCTTCGGA AGAAGGCGCT ACGTGCCCGA CCTCAACGCC CGGGTGAAGA      2220
GCGTCAGGGA GGCCGCGGAG CGCATGGCCT TCAACATGCC CGTCCAGGGC ACCGCCGCCG      2280
ACCTCATGAA GCTCGCCATG GTGAAGCTCT TCCCCGCCT CCGGGAGATG GGGGCCCGCA      2340
TGCTCCTCCA GGTCCACGAC GAGCTCCTCC TGGAGGCCCC CCAAGCGCGG GCCGAGGAGG      2400
TGGCGGCTTT GGCCAAGGAG GCCATGGAGA AGGCCTATCC CCTCGCCGTG CCCCTGGAGG      2460
TGGAGGTGGG GATGGGGGAG GACTGGCTTT CCGCCAAGGG TTAG                          2504

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 832 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu
1              5              10              15

Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly
                20              25              30

Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
          35              40              45

Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val
          50              55              60

Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly
65              70              75              80

Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
          85              90              95

Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu
          100             105             110

Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
          115             120             125

Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
          130             135             140

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Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	485	490	495
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	500	505	510
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	515	520	525
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	530	535	540
Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	Leu	545	550	555
His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	565	570	575
Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	580	585	590
Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	Ala	595	600	605
Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	610	615	620
Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	625	630	635
Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	645	650	655
Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	660	665	670
Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	675	680	685
Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	690	695	700
Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	705	710	715
Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	725	730	735
Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	740	745	750
Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	755	760	765
Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	770	775	780

Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
785					790					795					800
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
			805						810					815	
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu
			820					825					830		

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 831 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1			5						10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
		20					25						30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35				40						45			
Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Val	Val	Val	Val	Val
	50					55				60					
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala	Tyr
65				70						75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
			85						90					95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Val	Arg	Leu	Glu	Val
		100					105						110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Arg	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ala	Ile	Leu	His	Pro	Glu	Gly	Tyr
145				150						155					160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Tyr	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu
			165						170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
		180						185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Gln	Arg	Leu	Ile	Arg
		195					200					205			

Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Phe	Gln	His	Leu	Asp	Gln	Val	Lys	210	215	220
Pro	Ser	Leu	Arg	Glu	Lys	Leu	Gln	Ala	Gly	Met	Glu	Ala	Leu	Ala	Leu	225	230	235
Ser	Arg	Lys	Leu	Ser	Gln	Val	His	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp	245	250	255
Phe	Gly	Arg	Arg	Arg	Thr	Pro	Asn	Leu	Glu	Gly	Leu	Arg	Ala	Phe	Leu	260	265	270
Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	Glu	275	280	285
Gly	Pro	Lys	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	290	295	300
Phe	Leu	Gly	Phe	Ser	Phe	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	305	310	315
Leu	Ala	Leu	Ala	Gly	Ala	Trp	Glu	Gly	Arg	Leu	His	Arg	Ala	Gln	Asp	325	330	335
Pro	Leu	Arg	Gly	Leu	Arg	Asp	Leu	Lys	Gly	Val	Arg	Gly	Ile	Leu	Ala	340	345	350
Lys	Asp	Leu	Ala	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Asp	Leu	Phe	Pro	355	360	365
Glu	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	370	375	380
Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp	385	390	395
Ala	Gly	Glu	Arg	Ala	Leu	Leu	Ala	Glu	Arg	Leu	Phe	Gln	Thr	Leu	Lys	405	410	415
Glu	Arg	Leu	Lys	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Glu	Glu	Val	420	425	430
Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	Arg	Met	Glu	Ala	Thr	Gly	Val	435	440	445
Arg	Leu	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Val	Glu	Ala	450	455	460
Glu	Val	Arg	Gln	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	465	470	475
Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	485	490	495
Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	Ser	500	505	510
Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	515	520	525
Asp	Arg	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr	530	535	540

Ile	Asp	Pro	Leu	Pro	Ala	Leu	Val	His	Pro	Lys	Thr	Gly	Arg	Leu	His	545	550	555									560
Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser		565	570								575	
Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg		580	585								590	
Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Val	Leu	Val	Val	Leu		595	600								605	
Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp		610	615								620	
Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	Thr	Gln		625	630								640	
Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Ser	Pro	Glu	Gly	Val	Asp	Pro	Leu		645	650								655	
Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met		660	665								670	
Ser	Ala	His	Arg	Leu	Ser	Gly	Glu	Leu	Ser	Ile	Pro	Tyr	Glu	Glu	Ala		675	680								685	
Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Tyr	Pro	Lys	Val	Arg	Ala		690	695								700	
Trp	Ile	Glu	Gly	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu		705	710								720	
Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val		725	730								735	
Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val		740	745								750	
Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Arg	Leu	Phe		755	760								765	
Pro	Arg	Leu	Gln	Glu	Leu	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His	Asp		770	775								780	
Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Asp	Arg	Ala	Glu	Arg	Val	Ala	Ala		785	790								800	
Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Trp	Pro	Leu	Gln	Val	Pro	Leu		805	810								815	
Glu	Val	Glu	Val	Gly	Leu	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu			820	825								830	

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 834 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	
1				5					10					15		
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	
			20					25					30			
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	
			35				40					45				
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe	
	50					55					60					
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	
65					70					75					80	
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	
			100					105					110			
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	
		115					120					125				
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	
	130					135					140					
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu	
145					150					155					160	
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
			165						170					175		
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	
			180					185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu	
		195					200					205				
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp	
225				230						235					240	
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu	
			245						250					255		
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg	
			260					265					270			
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	
		275					280					285				
Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	
	290					295					300					

Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys 325	Ala	Leu	Ala	Ala	Cys 330	Arg	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg 395	Arg	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly 425	Glu	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr	Gly 450	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln 460	Ala	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe 485	Asn	Leu	Asn	Ser	Arg 490	Asp	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro	Ile 530	Val	Glu	Lys	Ile	Leu	Gln 535	His	Arg	Glu	Leu	Thr 540	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro 550	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560
Arg	Leu	His	Thr 565	Arg	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln 585	Asn	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATGNNGGCGA TGCTTCCCCT CTTTGAGCCC AAAGGCCGGG TCCTCCTGGT GGACGGCCAC	60
CACCTGGCCT ACCGCACCTT CTCGCCCTG AAGGGCCTCA CCACCAGCCG GGGCGAACCG	120
GTGCAGGCGG TCTACGGCTT CGCCAAGAGC CTCCTCAAGG CCCTGAAGGA GGACGGGGAC	180
MNGGCGGTGN TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGAG	240
GCCTACAAGG CGGGCCGGGC CCCCACCCCG GAGGACTTTC CCCGGCAGCT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTTGCG CGCCTCGAGG TCCCCGGCTA CGAGGCGGAC	360

GACGTNCTGG	CCACCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GGTACGAGGT	GCGCATCCTC	420
ACCGCCGACC	GCGACCTCTA	CCAGCTCCTT	TCCGACCGCA	TCGCCGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	GTGGCTTTGG	GAGAAAGTACG	GCCTGAGGCC	GGAGCAGTGG	540
GTGGACTACC	GGGCCCTGGC	GGGGGACCCC	TCCGACAACC	TCCCCGGGGT	CAAGGGCATC	600
GGGGAGAAGA	CCGCCCNGAA	GCTCCTCNAG	GAGTGGGGGA	GCCTGGAAAA	CCTCCTCAAG	660
AACCTGGACC	GGGTGAAGCC	CGCCNTCCGG	GAGAAGATCC	AGGCCACAT	GGANGACCTG	720
ANGCTCTCCT	GGGAGCTNTC	CCAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAGNGGCGGG	AGCCCGACCG	GGAGGGGCTT	AGGGCCTTTC	TGGAGAGGCT	GGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTTCG	CCTCCTGGAG	GGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCTT	CGTGGGCTTT	GTCTTTTCCC	GCCCCGAGCC	CATGTGGGCC	960
GAGCTTCTGG	CCCTGGCCGC	CGCCAGGGAG	GGCCGGGTCC	ACCGGGCACC	AGACCCCTTT	1020
ANGGGCCTNA	GGGACCTNAA	GGAGGTGCGG	GGNCTCCTCG	CCAAGGACCT	GGCCGTTTTG	1080
GCCCTGAGGG	AGGGCCTNGA	CCTCNTGCC	GGGGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCCT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGGGG	GGAGTGGACG	1200
GAGGANGCGG	GGGAGCGGGC	CCTCCTNTCC	GAGAGGCTCT	TCCNGAACCT	NNNGCAGCGC	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCAGGAGG	TGGAGAAGCC	CCTTTCCCGG	1320
GTCTTGCCCC	ACATGGAGGC	CACGGGGGTN	CGGCTGGACG	TGGCCTACCT	CCAGGCCCTN	1380
TCCCTGGAGG	TGGCGGAGGA	GATCCGCCGC	CTCGAGGAGG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TGCTCTTTGA	CGAGCTNGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACN	GGCAAGCGCT	CCACCAGCGC	CGCCGTGCTG	1560
GAGGCCCTNC	GNGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTCAAGA	ACACCTACAT	NGACCCCTTG	CCNGNCCTCG	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTTAGTAG	CTCCGACCCC	1740
AACCTGCAGA	ACATCCCCGT	CCGCACCCCN	CTGGGCCAGA	GGATCCGCCG	GGCCTTCGTG	1800
GCCGAGGAGG	GNTGGGTGTT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CCGGGTCTCTG	1860
GCCCACCTCT	CCGGGGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGAG	GGACATCCAC	1920
ACCCAGACCG	CCAGCTGGAT	GTTCCGGCGTC	CCCCCGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCCGCCCA	CCGCCTCTCC	2040
CAGGAGCTTG	CCATCCCCTA	CGAGGAGGCG	GTGGCCTTCA	TTGAGCGCTA	CTTCCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGGCGCTAC	GTGCCCAGCC	TCAACGCCCC	GGTGAAGAGC	2220

GTGCGGGAGG CGGCGGAGCG CATGGCCTTC AACATGCCCCG TCCAGGGCAC CGCCGCCGAC	2280
CTCATGAAGC TGGCCATGGT GAAGCTCTTC CCCC GGCTNC AGGAAATGGG GGCCAGGATG	2340
CTCCTNCAGG TCCACGACGA GCTGGTCCTC GAGGCCCCCA AAGAGCGGGC GGAGGNGGTG	2400
GCCGCTTTGG CCAAGGAGGT CATGGAGGGG GTCTATCCCC TGGCCGTGCC CCTGGAGGTG	2460
GAGGTGGGGA TGGGGGAGGA CTGGCTCTCC GCCAAGGAGT AG	2502

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 833 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 63
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 109
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 186
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 205
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 209
- (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 227..228
- (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 233
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 240
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 243..244
 (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 247
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 260
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 290
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 329
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 336
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 340
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 368
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 414
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 417..418
 (D) OTHER INFORMATION: /note= "Xaa at these positions can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 431
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 551
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 605
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 773
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 794
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 798
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 823
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(ix) FEATURE:
 (A) NAME/KEY: Modified-site
 (B) LOCATION: 833
 (D) OTHER INFORMATION: /note= "Xaa at this position can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Xaa	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1			5					10					15		
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
		20					25					30			
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
		35				40					45				
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Xaa	Val
	50					55				60					
Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu	Ala
65				70					75					80	
Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu
			85						90					95	
Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Xaa	Arg	Leu	Glu
			100					105					110		
Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys
		115					120					125			
Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp
	130					135					140				
Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	Ala	Val	Leu	His	Pro	Glu	Gly
145					150					155					160
Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro
				165					170					175	
Glu	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Xaa	Gly	Asp	Pro	Ser	Asp	Asn
			180					185					190		
Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Xaa	Lys	Leu	Leu
		195					200					205			
Xaa	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Val
	210					215					220				
Lys	Pro	Xaa	Xaa	Arg	Glu	Lys	Ile	Xaa	Ala	His	Met	Glu	Asp	Leu	Xaa
225					230					235					240
Leu	Ser	Xaa	Xaa	Leu	Ser	Xaa	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val
				245					250					255	
Asp	Phe	Ala	Xaa	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg	Ala	Phe
			260					265					270		
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu
		275					280					285			
Glu	Xaa	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly
	290					295					300				
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu
305					310					315					320

Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
 325 330 335
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
 405 410 415
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830
 Xaa

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1647 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTTGG CCAGCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420

ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGA CTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GCGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCGCT	1320
GTCTTGCCC ACATGGAGGC CACGGGGGTG CGCTTGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAGGG TCCTCTTTGA CGAGCTAGGG	1500
CTTCCCGCCA TCGGCAAGAC GGAGAAGACC GGCAAGCGCT CCACCAGCGC CGCCGTCCTG	1560
GAGGCCCTCC GCGAGGCCCA CCCCATCGTG GAGAAGATCC TGCAGGCATG CAAGCTTGGC	1620
ACTGGCCGTC GTTTTACAAC GTCGTGA	1647

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2088 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCAAGGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTGCGCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCTACGGG	240

GGGTACAAGG	CGGGCCGGGC	CCCCACGCCG	GAGGACTTTC	CCCGGCAACT	CGCCCTCATC	300
AAGGAGCTGG	TGGACCTCCT	GGGGCTGGCG	CGCCTCGAGG	TCCCGGGCTA	CGAGGCGGAC	360
GACGTCCTGG	CCAGCCTGGC	CAAGAAGGCG	GAAAAGGAGG	GCTACGAGGT	CCGCATCCTC	420
ACCGCCGACA	AAGACCTTTA	CCAGCTCCTT	TCCGACCGCA	TCCACGTCCT	CCACCCCGAG	480
GGGTACCTCA	TCACCCCGGC	CTGGCTTTGG	GAAAAGTACG	GCCTGAGGCC	CGACCAGTGG	540
GCCGACTACC	GGGCCCTGAC	CGGGGACGAG	TCCGACAACC	TCCCGGGGT	CAAGGGCATC	600
GGGAGAAGA	CGGCGAGGAA	GCTTCTGGAG	GAGTGGGGGA	GCCTGGAAGC	CCTCCTCAAG	660
AACCTGGACC	GGCTGAAGCC	CGCCATCCGG	GAGAAGATCC	TGGCCACAT	GGACGATCTG	720
AAGCTCTCCT	GGGACCTGGC	CAAGGTGCGC	ACCGACCTGC	CCCTGGAGGT	GGACTTCGCC	780
AAAAGGCGGG	AGCCCGACCG	GGAGAGGCTT	AGGGCCTTTC	TGGAGAGGCT	TGAGTTTGGC	840
AGCCTCCTCC	ACGAGTTCGG	CCTTCTGGAA	AGCCCCAAGG	CCCTGGAGGA	GGCCCCCTGG	900
CCCCCGCCGG	AAGGGGCCCTT	CGTGGGCTTT	GTGCTTTCCC	GCAAGGAGCC	CATGTGGGCC	960
GATCTTCTGG	CCCTGGCCGC	CGCCAGGGGG	GGCCGGGTCC	ACCGGGCCCC	CGAGCCTTAT	1020
AAAGCCCTCA	GGGACCTGAA	GGAGGCGCGG	GGGCTTCTCG	CCAAAGACCT	GAGCGTTCTG	1080
GCCCTGAGGG	AAGGCCCTTG	CCTCCCGCCC	GGCGACGACC	CCATGCTCCT	CGCCTACCTC	1140
CTGGACCCTT	CCAACACCAC	CCCCGAGGGG	GTGGCCCGGC	GCTACGGCGG	GGAGTGGACG	1200
GAGGAGGCGG	GGGAGCGGGC	CGCCCTTTCC	GAGAGGCTCT	TCGCCAACCT	GTGGGGGAGG	1260
CTTGAGGGGG	AGGAGAGGCT	CCTTTGGCTT	TACCGGGAGG	TGGAGAGGCC	CCTTTCCGCT	1320
GTCTTGCCC	ACATGGAGGC	CACGGGGGTG	CGCCTGGACG	TGGCCTATCT	CAGGGCCTTG	1380
TCCCTGGAGG	TGGCCGGGGA	GATCGCCCGC	CTCGAGGCCG	AGGTCTTCCG	CCTGGCCGGC	1440
CACCCCTTCA	ACCTCAACTC	CCGGGACCAG	CTGGAAAGGG	TCCTCTTTGA	CGAGCTAGGG	1500
CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCAG	GACGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTGCGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCCTCTCC	2040
CAGGAGCTAG	CTAGCCATCC	CTTACGAGGA	GGCCCAGGCC	TTCATTGA		2088

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCCTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTTGG CCAGCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCTTC	420
ACCGCCGACA AAGACCTTTA CCAGCTTCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCAGTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGA CTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGT CATGGAGGGG GTGTATCCCC	900
TGGCCGTGCC CCTGGAGGTG GAGGTGGGGA TAGGGGAGGA CTGGCTCTCC GCCAAGGAGT	960
GA	962

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATGGAATTCG	GGGATGCTGC	CCCTCTTTGA	GCCCAAGGGC	CGGGTCCTCC	TGGTGGACGG	60
CCACCACCTG	GCCTACCGCA	CCTTCCACGC	CCTGAAGGGC	CTCACCACCA	GCCGGGGGGA	120
GCCGGTGCAG	GCGGTCTACG	GCTTCGCCAA	GAGCCTCCTC	AAGGCCCTCA	AGGAGGACGG	180
GGACGCGGTG	ATCGTGGTCT	TTGACGCCAA	GGCCCCCTCC	TTCCGCCACG	AGGCCTACGG	240
GGGGTACAAG	GCGGGCCGGG	CCCCCACGCC	GGAGGACTTT	CCCCGGCAAC	TCGCCCTCAT	300
CAAGGAGCTG	GTGGACCTCC	TGGGGCTGGC	GCGCCTCGAG	GTCCCGGGCT	ACGAGGCGGA	360
CGACGTCCTG	GCCAGCCTGG	CCAAGAAGGC	GGAAAAGGAG	GGCTACGAGG	TCCGCATCCT	420
CACCGCCGAC	AAAGACCTTT	ACCAGCTCCT	TTCCGACCGC	ATCCACGTCC	TCCACCCCGA	480
GGGGTACCTC	ATCACCCCGG	CCTGGCTTTG	GGAAAAGTAC	GGCCTGAGGC	CCGACCAGTG	540
GGCCGACTAC	CGGGCCCTGA	CCGGGGACGA	GTCCGACAAC	CTTCCCGGGG	TCAAGGGCAT	600
CGGGGAGAAG	ACGGCGAGGA	AGCTTCTGGA	GGAGTGGGGG	AGCCTGGAAG	CCCTCCTCAA	660
GAACCTGGAC	CGGCTGAAGC	CCGCCATCCG	GGAGAAGATC	CTGGCCCACA	TGGACGATCT	720
GAAGCTCTCC	TGGGACCTGG	CCAAGGTGCG	CACCGACCTG	CCCCTGGAGG	TGGACTTCGC	780
CAAAAGGCGG	GAGCCCCGAC	GGGAGAGGCT	TAGGGCCTTT	CTGGAGAGGC	TTGAGTTTGG	840
CAGCCTCCTC	CACGAGTTCG	GCCTTCTGGA	AAGCCCCAAG	ATCCGCCGGG	CCTTCATCGC	900
CGAGGAGGGG	TGGCTATTGG	TGGCCCTGGA	CTATAGCCAG	ATAGAGCTCA	GGGTGCTGGC	960
CCACCTCTCC	GGCGACGAGA	ACCTGATCCG	GGTCTTCCAG	GAGGGGCGGG	ACATCCACAC	1020
GGAGACCGCC	AGCTGGATGT	TCGGCGTCCC	CCGGGAGGCC	GTGGACCCCC	TGATGCGCCG	1080
GGCGGCCAAG	ACCATCAACT	TCGGGGTCCT	CTACGGCATG	TCGGCCCACC	GCCTCTCCCA	1140
GGAGCTAGCC	ATCCCTTACG	AGGAGGCCCA	GGCCTTCATT	GAGCGCTACT	TTCAGAGCTT	1200
CCCCAAGGTG	CGGGCCTGGA	TTGAGAAGAC	CCTGGAGGAG	GGCAGGAGGC	GGGGGTACGT	1260
GGAGACCCTC	TTCGGCCGCC	GCCGCTACGT	GCCAGACCTA	GAGGCCCGGG	TGAAGAGCGT	1320
GCGGGAGGCG	GCCGAGCGCA	TGGCCTTCAA	CATGCCCCGTC	CGGGGCACCG	CCGCCGACCT	1380
CATGAAGCTG	GCTATGGTGA	AGCTCTTCCC	CAGGCTGGAG	GAAATGGGGG	CCAGGATGCT	1440
CCTTCAGGTC	CACGACGAGC	TGGTCCTCGA	GGCCCCAAAA	GAGAGGGCGG	AGGCCGTGGC	1500
CCGGCTGGCC	AAGGAGGTCA	TGGAGGGGGT	GTATCCCCTG	GCCGTGCCCC	TGGAGGTGGA	1560
GGTGGGGATA	GGGGAGGACT	GGCTCTCCGC	CAAGGAGTGA			1600

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACGAATTCG GGGATGCTGC CCCTCTTTGA GCCCAA 36

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGATCTA TCACTCCTTG GCGGAGAGCC AGTC 34

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAGCTCGC CCGGGCGAGC TCGAATTCCG 60

TGTATTCTAT AGTGTCACCT AAATCGAATT C 91

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAATACGACT CACTATAGGG 20

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTCGATT TAGGTGACAC TATAGAA 27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GTAATCATGG TCATAGCTGG TAGCTTGCTA C 31

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATCCTCTA GAGTCGACCT GCAGGCATGC CTACCTTGGT AG 42

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGATCCTCTA GAGTCGACCT GCAGGCATGC 30

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATGAATTCGG GGATGCTGCC CCTCTTTGAG CCCAAGGGCC GGGTCCTCCT GGTGGACGGC	60
CACCACCTGG CCTACCGCAC CTTCCACGCC CTGAAGGGCC TCACCACCAG CCGGGGGGAG	120
CCGGTGCAGG CGGTCTACGG CTTCGCCAAG AGCCTCCTCA AGGCCCTCAA GGAGGACGGG	180
GACGCGGTGA TCGTGGTCTT TGACGCCAAG GCCCCCTCCT TCCGCCACGA GGCTTACGGG	240
GGGTACAAGG CGGGCCGGGC CCCACGCCG GAGGACTTTC CCCGGCAACT CGCCCTCATC	300
AAGGAGCTGG TGGACCTCCT GGGGCTGGCG CGCCTCGAGG TCCCGGGCTA CGAGGCGGAC	360
GACGTCTTGG CCAGCTGGC CAAGAAGGCG GAAAAGGAGG GCTACGAGGT CCGCATCCTC	420
ACCGCCGACA AAGACCTTTA CCAGCTCCTT TCCGACCGCA TCCACGTCCT CCACCCCGAG	480
GGGTACCTCA TCACCCCGGC CTGGCTTTGG GAAAAGTACG GCCTGAGGCC CGACCACTGG	540
GCCGACTACC GGGCCCTGAC CGGGGACGAG TCCGACAACC TTCCCGGGGT CAAGGGCATC	600
GGGGAGAAGA CGGCGAGGAA GCTTCTGGAG GAGTGGGGGA GCCTGGAAGC CCTCCTCAAG	660
AACCTGGACC GGCTGAAGCC CGCCATCCGG GAGAAGATCC TGGCCCACAT GGACGATCTG	720
AAGCTCTCCT GGGACCTGGC CAAGGTGCGC ACCGACCTGC CCCTGGAGGT GGACTTTCGCC	780
AAAAGGCGGG AGCCCGACCG GGAGAGGCTT AGGGCCTTTC TGGAGAGGCT TGAGTTTGGC	840
AGCCTCCTCC ACGAGTTCGG CCTTCTGGAA AGCCCCAAGG CCCTGGAGGA GGCCCCCTGG	900
CCCCCGCCGG AAGGGGCCTT CGTGGGCTTT GTGCTTTCCC GCAAGGAGCC CATGTGGGCC	960
GATCTTCTGG CCCTGGCCGC CGCCAGGGGG GGCCGGGTCC ACCGGGCCCC CGAGCCTTAT	1020
AAAGCCCTCA GGGACCTGAA GGAGGCGCGG GGGCTTCTCG CCAAAGACCT GAGCGTTCTG	1080
GCCCTGAGGG AAGGCCTTGG CCTCCCGCCC GCGGACGACC CCATGCTCCT CGCCTACCTC	1140
CTGGACCCTT CCAACACCAC CCCCAGGGGG GTGGCCCGGC GCTACGGCGG GGAGTGGACG	1200
GAGGAGGCGG GGGAGCGGGC CGCCCTTTCC GAGAGGCTCT TCGCCAACCT GTGGGGGAGG	1260
CTTGAGGGGG AGGAGAGGCT CCTTTGGCTT TACCGGGAGG TGGAGAGGCC CCTTTCCTCT	1320
GTCTTGCCCC ACATGGAGGC CACGGGGGTG CGCCTGGACG TGGCCTATCT CAGGGCCTTG	1380
TCCCTGGAGG TGGCCGGGGA GATCGCCCGC CTCGAGGCCG AGGTCTTCCG CCTGGCCGGC	1440
CACCCCTTCA ACCTCAACTC CCGGGACCAG CTGGAAAGGG TCCTCTTTGA CGAGCTAGGG	1500

CTTCCCGCCA	TCGGCAAGAC	GGAGAAGACC	GGCAAGCGCT	CCACCAGCGC	CGCCGTCCTG	1560
GAGGCCCTCC	GCGAGGCCCA	CCCCATCGTG	GAGAAGATCC	TGCAGTACCG	GGAGCTCACC	1620
AAGCTGAAGA	GCACCTACAT	TGACCCCTTG	CCGGACCTCA	TCCACCCCAG	GACGGGGCCGC	1680
CTCCACACCC	GCTTCAACCA	GACGGCCACG	GCCACGGGCA	GGCTAAGTAG	CTCCGATCCC	1740
AACCTCCAGA	ACATCCCCGT	CCGCACCCCG	CTTGGGCAGA	GGATCCGCCG	GGCCTTCATC	1800
GCCGAGGAGG	GGTGGCTATT	GGTGGCCCTG	GACTATAGCC	AGATAGAGCT	CAGGGTGCTG	1860
GCCCACCTCT	CCGGCGACGA	GAACCTGATC	CGGGTCTTCC	AGGAGGGGCG	GGACATCCAC	1920
ACGGAGACCG	CCAGCTGGAT	GTTGCGCGTC	CCCCGGGAGG	CCGTGGACCC	CCTGATGCGC	1980
CGGGCGGCCA	AGACCATCAA	CTTCGGGGTC	CTCTACGGCA	TGTCGGCCCA	CCGCTCTCTC	2040
CAGGAGCTAG	CCATCCCTTA	CGAGGAGGCC	CAGGCCTTCA	TTGAGCGCTA	CTTTCAGAGC	2100
TTCCCCAAGG	TGCGGGCCTG	GATTGAGAAG	ACCCTGGAGG	AGGGCAGGAG	GCGGGGGTAC	2160
GTGGAGACCC	TCTTCGGCCG	CCGCCGCTAC	GTGCCAGACC	TAGAGGCCCG	GGTGAAGAGC	2220
GTGCGGGAGG	CGGCCGAGCG	CATGGCCTTC	AACATGCCCG	TCCGGGGCAC	CGCCGCCGAC	2280
CTCATGAAGC	TGGCTATGGT	GAAGCTCTTC	CCCAGGCTGG	AGGAAATGGG	GGCCAGGATG	2340
CTCCTTCAGG	TCCACGACGA	GCTGGTCCTC	GAGGCCCCAA	AAGAGAGGGC	GGAGGCCGTG	2400
GCCCGGCTGG	CCAAGGAGGT	CATGGAGGGG	GTGTATCCCC	TGGCCGTGCC	CCTGGAGGTG	2460
GAGGTGGGGA	TAGGGGAGGA	CTGGCTCTCC	GCCAAGGAGT	GA		2502

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATTTAGGTG AACTATAG

19

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGGACGAACA AGCGAGACAG CGACACAGGT ACCACATGGT ACAAGAGGCA AGAGAGACGA 60

CACAGCAGAA AC 72

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GTTTCTGCTG TGTCGTCTCT CTTGCCTCTT GTACCATGTG GTACCTGTGT CGCTGTCTCG 60

CTTGTTTCGTC 70

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTTTCTGCTG TGTCGTCTCT CTTG 24

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTCTTGTTAC CATGTGGTAC CTGTGTCGCT GTCTCGCTTG TTCGTC 46

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ACACAGGTAC CACATGGTAC AAGAGGCAAG AGAGACGACA CAGCAGAAAC 50

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser

1 5 10 15

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 969 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCGGATCA ATTCGGGGAT GCTGCCCCTC 60

TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC 120

CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC 180

GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC 240

GCCAAGGCCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC 300

ACGCCGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGG CCTCCTGGGG 360

CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG 420

AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG 480

CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG 540

CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCCCT GGAGGTGGAC TTCGCCAAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGTCATG GAGGGGTGT ATCCCTGGC CGTGCCCTG GAGGTGGAGG	960
TGGGGATAG	969

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 948 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATGGCTAGCA TGACTGGTGG ACAGCAAATG GGTCCGATCA ATTCGGGGAT GCTGCCCCCTC	60
TTTGAGCCCA AGGGCCGGGT CCTCCTGGTG GACGGCCACC ACCTGGCCTA CCGCACCTTC	120
CACGCCCTGA AGGGCCTCAC CACCAGCCGG GGGGAGCCGG TGCAGGCGGT CTACGGCTTC	180
GCCAAGAGCC TCCTCAAGGC CCTCAAGGAG GACGGGGACG CGGTGATCGT GGTCTTTGAC	240
GCCAAGGCC CCTCCTTCCG CCACGAGGCC TACGGGGGGT ACAAGGCGGG CCGGGCCCCC	300
ACGCCGGAGG ACTTTCCCCG GCAACTCGCC CTCATCAAGG AGCTGGTGGA CCTCCTGGGG	360
CTGGCGCGCC TCGAGGTCCC GGGCTACGAG GCGGACGACG TCCTGGCCAG CCTGGCCAAG	420
AAGGCGGAAA AGGAGGGCTA CGAGGTCCGC ATCCTCACCG CCGACAAAGA CCTTTACCAG	480
CTTCTTTCCG ACCGCATCCA CGTCCTCCAC CCCGAGGGGT ACCTCATCAC CCCGGCCTGG	540
CTTTGGGAAA AGTACGGCCT GAGGCCCGAC CAGTGGGCCG ACTACCGGGC CCTGACCGGG	600
GACGAGTCCG ACAACCTTCC CGGGGTCAAG GGCATCGGGG AGAAGACGGC GAGGAAGCTT	660
CTGGAGGAGT GGGGGAGCCT GGAAGCCCTC CTCAAGAACC TGGACCGGCT GAAGCCCGCC	720
ATCCGGGAGA AGATCCTGGC CCACATGGAC GATCTGAAGC TCTCCTGGGA CCTGGCCAAG	780
GTGCGCACCG ACCTGCCCCCT GGAGGTGGAC TTCGCCAAAA GGCGGGAGCC CGACCGGGAG	840
AGGCTTAGGG CCTTTCTGGA GAGGCTTGAG TTTGGCAGCC TCCTCCACGA GTTCGGCCTT	900
CTGGAAAGCC CCAAGGCCGC ACTCGAGCAC CACCACCACC ACCACTGA	948

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCCAGGGTT TTCCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTCTGGGTTT TCTGCTCTCT GGTCGCTGTC TCGCTTGTTT GTC	43
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(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCTGTCTCGC TTGTTTCGTC	19
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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
GACGAACAAG CGAGACAGCG 20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
TTCTGGGTTC TCTGCTCTCT GGTC 24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:
GACGAACAAG CGAGACAGCG ACCAGAGAGC AGAGAACCCA GAA 43

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:
ACCAGAGAGC AGAGAACCCA GAA 23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
AACAGCTATG ACCATGATTA C 21

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAG	157

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAG	157

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CACCGTCCTC TTCAAGAAG	19
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(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTGAATCTTG TAGATAGCTA 20

(2) INFORMATION FOR SEQ ID NO:44

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GCCTTATTTT ACTTTAAAAA TTTTCAAATG TTTCTTTTAT ACACAATATG TTTCTTAGTC 60

TGAATAACCT TTTCTCTGCT AGTATTTTGT AGCAGTGGCT CCGAAGGCAC CGTCCTCTTC 120

AAGAAGTTTA TCCAGAAGCC AATGCACCCA TTAGACATAA CCGGGAATCC TACATGGTTC 180

CTTTTATACC ACTGTACAGA AATGGTGATT TCTTTATTTT ATCCAAAGAT CTGGGCTATG 240

ACTATAGCTA TCTACAAGAT TCAGGTAAAG TTTACTTTCT TTCAGAGGAA TTGCTGAATC 300

TAGTGTTACC AATTTATTTT GAGATAACAC AAAACTTTA 339

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GCCTTATTTT ACTTTAAAAA T 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TAAAGTTTTG TGTTATCTCA 20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTGAG	157

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CCAATGGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AGCGGATAAC AATTTACAC AGGAAACAGC TATGACCATG ATTACGCCAA GCTATTTAGG	60
TGACACTATA GAATACTCAA GCTTGCATGC CTGCAGGTCG ACTCTAGAGG ATCCCCGGGT	120
ACCGAGCTCG AATTCGCCCT ATAGTGAGTC GTATTAGGAT CCGTG	165

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCCTGTGT GAAATTGTTA TCCGCT	206

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

AGCGGATAAC AATTTCACAC AGGA	24
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(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CACGGATCCT AATACGACTC ACTATAGGG	29
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(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CGCCAGGGTT TTCCAGTCA CGAC	24
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(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTAGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG	157

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCGGGAA	60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA	120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAGACC CAGACTCTTT TCAAGACTAC	180
ATTAAGTCCT ATTTGGAACA AGCGAGTCGG ATCTGGTCAT GGCTCCTTGG GGCGGCGATG	240
GTAGGGGCCG TCCTCACTGC CCTGCTGGCA GGGCTTGTGA GCTTGCTGTG TCGTCACAAG	300
AGAAAGCAGC TTCCTGAAGA AAAGCAGCCA CTCCTCATGG AGAAAGAGGA TTACCACAGC	360
TTGTATCAGA GCCATTTA	378

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACCGTCCTC	TTCAAGAAGT	TTATCCAGAA	GCCAATGCAC	CCATTGGACA	TAACCAGGAA	60
TCCTACATGG	TTCTTTTAT	ACCACTGTAC	AGAAATGGTG	ATTTCTTTAT	TTCATCCAAA	120
GATCTGGGCT	ATGACTATAG	CTATCTACAA	GATTCAGACC	CAGACTCTTT	TCAAGACTAC	180
ATTAAGTCCT	ATTTGGAACA	AGCGAGTCGG	ATCTGGTCAT	GGCTCCTTGG	GGCGGCGATG	240
GTAGGGGCCG	TCCTCACTGC	CCTGCTGGCA	GGGCTTGTGA	GCTTGCTGTG	TCGTCACAAG	300
AGAAAGCAGC	TTCTGAAGA	AAAGCAGCCA	CTCCTCATGG	AGAAAGAGGA	TTACCACAGC	360
TTGTATCAGA	GCCATTTA					378

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1059 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GCAAGTTTGG	CTTTTGGGGA	CCAAACTGCA	CAGAGAGACG	ACTCTTGGTG	AGAAGAAACA	60
TCTTCGATTT	GAGTGCCCCA	GAGAAGGACA	AATTTTTTGC	CTACCTCACT	TTAGCAAAGC	120
ATACCATCAG	CTCAGACTAT	GTCATCCCCA	TAGGGACCTA	TGGCCAAATG	AAAAATGGAT	180
CAACACCCAT	GTTTAACGAC	ATCAATATTT	ATGACCTCTT	TGTCTGGATG	CATTATTATG	240
TGTCAATGGA	TGCACTGCTT	GGGGGATATG	AAATCTGGAG	AGACATTGAT	TTTGCCCATG	300
AAGCACCAGC	TTTTCTGCCT	TGGCATAGAC	TCTTCTTGTT	GCGGTGGGAA	CAAGAAATCC	360
AGAAGCTGAC	AGGAGATGAA	AACTTCACTA	TTCCATATTG	GGACTGGCGG	GATGCAGAAA	420
AGTGTGACAT	TTGCACAGAT	GAGTACATGG	GAGGTCAGCA	CCCCACAAAT	CCTAACTTAC	480
TCAGCCCAGC	ATCATCTTTC	TCCTCTTGGC	AGATTGTCTG	TAGCCGATTG	GAGGAGTACA	540
ACAGCCATCA	GTCTTTATGC	AATGGAACGC	CCGAGGGACC	TTTACGGCGT	AATCCTGGAA	600
ACCATGACAA	ATCCAGAACC	CCAAGGCTCC	CCTCTTCAGC	TGATGTAGAA	TTTTGCCTGA	660
GTTTGACCCA	ATATGAATCT	GGTTCCATGG	ATAAAGCTGC	CAATTCAGC	TTTAGAAATA	720
CACTGGAAGG	ATTTGCTAGT	CCACTTACTG	GGATAGCGGA	TGCCTCTCAA	AGCAGCATGC	780
ACAATGCCTT	GCACATCTAT	ATGAATGGAA	CAATGTCCCA	GGTACAGGGA	TCTGCCAACG	840
ATCCTATCTT	CCTTCTTCAC	CATGCATTTG	TTGACAGTAT	TTTGAGCAG	TGGCTCCGAA	900
GGCACCGTCC	TCTTCAAGAA	GTTTATCCAG	AAGCCAATGC	ACCCATTGGA	CATAACCGGG	960

AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG	1059

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1059 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCAAGTTTGG CTTTGGGGA CCAAAGTCA CAGAGAGACG ACTCTTGGTG AGAAGAAACA	60
TCTTCGATTT GAGTGCCCCA GAGAAGGACA AATTTTTTGC CTACCTCACT TTAGCAAAGC	120
ATACCATCAG CTCAGACTAT GTCATCCCCA TAGGGACCTA TGGCCAAATG AAAAATGGAT	180
CAACACCCAT GTTTAACGAC ATCAATATTT ATGACCTCTT TGTCTGGATG CATTATTATG	240
TGTCAATGGA TGCACTGCTT GGGGGATATG AAATCTGGAG AGACATTGAT TTTGCCCATG	300
AAGCACCAGC TTTTCTGCCT TGGCATAGAC TCTTCTTGTT GCGGTGGGAA CAAGAAATCC	360
AGAAGCTGAC AGGAGATGAA AACTTCACTA TTCCATATTG GGACTGGCGG GATGCAGAAA	420
AGTGTGACAT TTGCACAGAT GAGTACATGG GAGGTCAGCA CCCCACAAAT CCTAACTTAC	480
TCAGCCCAGC ATCATCTCTC TCCTCTTGGC AGATTGTCTG TAGCCGATTG GAGGAGTACA	540
ACAGCCATCA GTCTTTATGC AATGGAACGC CCGAGGGACC TTTACGGCGT AATCCTGGAA	600
ACCATGACAA ATCCAGAACC CCAAGGCTCC CCTCTTCAGC TGATGTAGAA TTTTGCCTGA	660
GTTTGACCCA ATATGAATCT GGTTCATGG ATAAAGCTGC CAATFTCAGC TTTAGAAATA	720
CACTGGAAGG ATTTGCTAGT CCACTTACTG GGATAGCGGA TGCCTCTCAA AGCAGCATGC	780
ACAATGCCTT GCACATCTAT ATGAATGGAA CAATGTCCCA GGTACAGGGA TCTGCCAACG	840
ATCCTATCTT CCTTCTTCAC CATGCATTTG TTGACAGTAT TTTTGAGCAG TGGCTCCGAA	900
GGCACCGTCC TCTTCAAGAA GTTTATCCAG AAGCCAATGC ACCCATTTGA CATAACCAGG	960
AATCCTACAT GGTTCCTTTT ATACCACTGT ACAGAAATGG TGATTTCTTT ATTTTCATCCA	1020
AAGATCTGGG CTATGACTAT AGCTATCTAC AAGATTCAG	1059

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1587 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ATGCTCCTGG CTGTTTTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTT	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTTGAG TGCCCCAGAG AAGGACAAAT TTTTGCCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTTCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGCACCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAATC CAGAACCCCA AGGCTCCCCT CTCAGCTGA TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080
AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCTCAGGT ACAGGGATCT	1140
GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG	1200
CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCGGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTATT	1320
TCATCCAAAG ATCTGGGCTA TGAATATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GCTCCTTGGG	1440
GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT	1500
CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT	1560
TACCACAGCT TGTATCAGAG CCATTTA	1587

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1587 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ATGCTCCTGG CTGTTTTGTA CTGCCTGCTG TGGAGTTTCC AGACCTCCGC TGGCCATTTTC	60
CCTAGAGCCT GTGTCTCCTC TAAGAACCTG ATGGAGAAGG AATGCTGTCC ACCGTGGAGC	120
GGGGACAGGA GTCCCTGTGG CCAGCTTTCA GGCAGAGGTT CCTGTCAGAA TATCCTTCTG	180
TCCAATGCAC CACTTGGGCC TCAATTTCCC TTCACAGGGG TGGATGACCG GGAGTCGTGG	240
CCTTCCGTCT TTTATAATAG GACCTGCCAG TGCTCTGGCA ACTTCATGGG ATTCAACTGT	300
GGAAACTGCA AGTTTGGCTT TTGGGGACCA AACTGCACAG AGAGACGACT CTTGGTGAGA	360
AGAAACATCT TCGATTGAG TGCCCCAGAG AAGGACAAAT TTTTTCCTA CCTCACTTTA	420
GCAAAGCATA CCATCAGCTC AGACTATGTC ATCCCCATAG GGACCTATGG CCAAATGAAA	480
AATGGATCAA CACCCATGTT TAACGACATC AATATTTATG ACCTCTTTGT CTGGATGCAT	540
TATTATGTGT CAATGGATGC ACTGCTTGGG GGATATGAAA TCTGGAGAGA CATTGATTTT	600
GCCCATGAAG CACCAGCTTT TCTGCCTTGG CATAGACTCT TCTTGTTGCG GTGGGAACAA	660
GAAATCCAGA AGCTGACAGG AGATGAAAAC TTCACTATTC CATATTGGGA CTGGCGGGAT	720
GCAGAAAAGT GTGACATTTG CACAGATGAG TACATGGGAG GTCAGACCCC CACAAATCCT	780
AACTTACTCA GCCCAGCATC ATTCTTCTCC TCTTGGCAGA TTGTCTGTAG CCGATTGGAG	840
GAGTACAACA GCCATCAGTC TTTATGCAAT GGAACGCCCC AGGGACCTTT ACGGCGTAAT	900
CCTGGAAACC ATGACAAAATC CAGAACCCCA AGGCTCCCCCT CTTCAGCTGA TGTAGAATTT	960
TGCCTGAGTT TGACCCAATA TGAATCTGGT TCCATGGATA AAGCTGCCAA TTTCAGCTTT	1020
AGAAATACAC TGGAAGGATT TGCTAGTCCA CTTACTGGGA TAGCGGATGC CTCTCAAAGC	1080
AGCATGCACA ATGCCTTGCA CATCTATATG AATGGAACAA TGTCCCAGGT ACAGGGATCT	1140
GCCAACGATC CTATCTTCCT TCTTCACCAT GCATTTGTTG ACAGTATTTT TGAGCAGTGG	1200
CTCCGAAGGC ACCGTCCTCT TCAAGAAGTT TATCCAGAAG CCAATGCACC CATTGGACAT	1260
AACCAGGAAT CCTACATGGT TCCTTTTATA CCACTGTACA GAAATGGTGA TTTCTTTTATT	1320
TCATCCAAAG ATCTGGGCTA TGACTATAGC TATCTACAAG ATTCAGACCC AGACTCTTTT	1380
CAAGACTACA TTAAGTCCTA TTTGGAACAA GCGAGTCGGA TCTGGTCATG GTCCTTGGG	1440

GCGGCGATGG TAGGGGCCGT CCTCACTGCC CTGCTGGCAG GGCTTGTGAG CTTGCTGTGT 1500
 CGTCACAAGA GAAAGCAGCT TCCTGAAGAA AAGCAGCCAC TCCTCATGGA GAAAGAGGAT 1560
 TACCACAGCT TGTATCAGAG CCATTTA 1587

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

TAAATGGCTC TGATACAAGC T 21

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCAAGTTTGG CTTTGGGGA 20

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ATGCTCCTGG CTGTTTGTGTA CTG 23

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CCGGTTATGT CTAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

CTGAATCTTG TAGATAGCTA TAGTCATAGC CCAGATCTTT GGATGAAATA AAGAAATCAC	60
CATTTCTGTA CAGTGGTATA AAAGGAACCA TGTAGGATTC CTGGTTATGT CCAATGGGTG	120
CATTGGCTTC TGGATAAACT TCTTGAAGAG GACGGTG	157

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGTTGGCCAA TCTACTCCCA GG	22
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(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GCTCACTCAG TGTGGCAAAG	20
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(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 536 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAGTGA CTCTCTGCCT ATTGGTCTAT TTTCCACCCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 534 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGGTCT GCCGTTACTG CCCTGTGGGG	180
CAAGGTGAAC GTGGATGAAG TTGGTGGTGA GGCCCTGGGC AGGTTGGTAT CAAGGTTACA	240
AGACAGGTTT AAGGAGACCA ATAGAAACTG GGCATGTGGA GACAGAGAAG ACTCTTGGGT	300
TTCTGATAGG CACTGACTCT CTCTGCCTAT TGGTCTATTT TCCCACCCTT AGGCTGCTGG	360
TGGTCTACCC TTGGACCCAG AGGTTCTTTG AGTCCTTTGG GGATCTGTCC ACTCCTGATG	420
CTGTTATGGG CAACCCTAAG GTGAAGGCTC ATGGCAAGAA AGTGCTCGGT GCCTTTAGTG	480
ATGGCCTGGC TCACCTGGAC AACCTCAAGG GCACCTTTGC CACACTGAGT GAGC	534

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCT AGAGGTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGAGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCCTGACT CTCTCTGCCT ATTGGTCTAT TTTCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAAUACUCAA GCUUGCAUGC CUGCAGGU CG ACUCUAGAGG AUCCCCGGGU ACCGAGCUCG 60

AAUU 64

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGCTGACAAG AAGGAAACTC 20

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CCAGGCGGCG GCTAGGAGAG ATGGG 25

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG 60

GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC 120

ATTTTCGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTT 180

TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC 240

CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC 300

ATTTTAGAAG TAGGCCAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G 351

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GATGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTAGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 340 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GGCTGACAAG AAGGAAACTC GCTGAGATAG CAGGGACTTT CCACAAGGGG ATGTTATGGG	60
GAGGAGCCGG TCGGGAACAC CCACTTTCTT GGTGTATAAA TATCACTGCA TTTCGCTCTG	120
TATTCAGTCG CTCTGCGGAG AGGCTGGCAG ATTGAGCCCT GGGAGGTTCT CTCCAGCACT	180
AGCAGGTAGA GCCTGGGTGT TCCCTGCTAG ACTCTCACCA GCACTTGGCC AGTGCTGGGC	240
AGAGTGGCTC CACGCTTGCT TGCTTAAAGA CCTCTTCAAT AAAGCTGCCA TTTTAGAAGT	300
AAGCCAGTGT GTGTTCCCAT CTCTCCTAGC CGCCGCCTGG	340

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 351 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCCCTCTCT TGATGTATAA ATATCACTGC	120
ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GGCTGACAAG AAGGAAACTC GCTGAAACAG CAGGGACTTT CCACAAGGGG ATGTTACGGG	60
GAGGTACTGG GAAGGAGCCG GTCGGGAACG CCCACTTTCT TGATGTATAA ATATCACTGC	120
ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TGGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGGGTG TTCCCTGCTA GACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGTGACT CCACGCTTGC TTGCTTAAAG CCCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAAGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GGCTGACAAG AAGGAAACTC GCTGAGACAG CAGGGACTTT CCACAAGGGG ATGTTACGGA	60
GAGGTACTGG GGAGGAGCCG GTCGGGAACG CCCACTCTCT TGATGTATAA ATATCACTGC	120
ATTTGCTCT GTATTCAGTC GCTCTGCGGA GAGGCTGGCA GATTGAGCCC TAGGAGGTTC	180
TCTCCAGCAC TAGCAGGTAG AGCCTGAGTG TTCCCTGCTA AACTCTCACC AGCACTTGGC	240
CGGTGCTGGG CAGAGCGGCT CCACGCTTGC TTGCTTAAAG ACCTCTTCAA TAAAGCTGCC	300
ATTTTAGAAG TAGGCTAGTG TGTGTTCCCA TCTCTCCTAG CCGCCGCCTG G	351

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA TCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT AAGGCCCTGG GCAGGTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAGTACT CTCTCTGCCT ATTGGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 536 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GGTTGGCCAA TCTACTCCCA GGAGCAGGGA GGGCAGGAGC CAGGGCTGGG CATAAAAGTC	60
AGGGCAGAGC CATCTATTGC TTACATTTGC TTCTGACACA ACTGTGTTCA CTAGCAACCT	120
CAAACAGACA CCATGGTGCA CCTGACTCCT GAGGAGAAGT CTGCCGTTAC TGCCCTGTGG	180
GGCAAGGTGA ACGTGGATGA AGTTGGTGGT GAGGCCCTGG GCAGGTGGT ATCAAGGTTA	240
CAAGACAGGT TTAAGGAGAC CAATAGAAAC TGGGCATGTG GAGACAGAGA AGACTCTTGG	300
GTTTCTGATA GGCAGTACT CTCTCTGCCT ATTAGTCTAT TTTCCCACCC TTAGGCTGCT	360
GGTGGTCTAC CCTTGGACCC AGAGGTTCTT TGAGTCCTTT GGGGATCTGT CCACTCCTGA	420
TGCTGTTATG GGCAACCCTA AGGTGAAGGC TCATGGCAAG AAAGTGCTCG GTGCCTTTAG	480
TGATGGCCTG GCTCACCTGG ACAACCTCAA GGGCACCTTT GCCACACTGA GTGAGC	536

(2) INFORMATION FOR SEQ ID NO:84:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
CACCGTCCTC TTCAAGAAGT TTATCCAGAA GCCAATGCAC CCATTGGACA TAACCAGGAA      60
TCCTACATGG TTCCTTTTAT ACCACTGTAC AGAAATGGTG ATTTCTTTAT TTCATCCAAA      120
GATCTGGGCT ATGACTATAG CTATCTACAA GATTCAG                                157
```

(2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 833 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1           5           10           15
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20          25          30
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35          40          45
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50          55          60
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65          70          75          80
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85          90          95
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100         105         110
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115         120         125
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130         135         140
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145         150         155         160
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165         170         175
```

Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
	225				230					235					240	
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
			245						250					255		
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
		260						265					270			
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	
	275						280					285				
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	
	290					295					300					
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	
	305				310					315					320	
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	
			325						330					335		
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	
			340					345					350			
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
	370					375					380					
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
	385				390					395					400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
			405						410					415		
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420					425					430			
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
	465				470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505						510		

Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Arg Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830
 Glu

(2) INFORMATION FOR SEQ ID NO:86:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 548 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	
1				5					10					15		
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	
			20					25					30			
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	
			35				40					45				
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	
	50					55					60					
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	
65					70					75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	
			100					105					110			
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
145					150					155					160	
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	
				165					170					175		
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	
		195					200					205				
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	
	210					215					220					
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	
225					230					235					240	
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	
				245					250					255		
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
			260					265					270			

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Ala Cys Lys Leu Gly Thr Gly Arg Arg
 530 535 540
 Phe Thr Thr Ser
 545

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 695 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
1				5					10					15	
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu
145					150					155					160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165						170					175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu
		195					200					205			
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
			245						250					255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala
			260					265					270		
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu
		275					280					285			
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu
	290					295					300				

Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	
305					310					315					320	
Asp	Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	
				325					330					335		
Pro	Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	
			340					345					350			
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
	370					375					380					
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
385					390					395					400	
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
				405					410					415		
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420					425					430			
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
465					470					475					480	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
			485						490					495		
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505					510			
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515				520						525				
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
545					550					555					560	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565					570					575		
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	
		595					600					605				
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	
	610					615					620					
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	
625					630					635					640	

Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
660 665 670

Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ser His Pro Leu
675 680 685

Arg Gly Gly Pro Gly Leu His
690 695

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 310 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
130 135 140

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
145 150 155 160

Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
165 170 175

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
180 185 190

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
195 200 205

Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro
 290 295 300
 Trp Arg Trp Arg Trp Gly
 305 310

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
 1 5 10 15
 Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 20 25 30
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
 35 40 45
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
 50 55 60
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
 65 70 75 80
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
 85 90 95
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
 100 105 110
 Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
 115 120 125
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
 130 135 140
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
 145 150 155 160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
 165 170 175
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
 180 185 190
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 195 200 205
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300
 Lys Ser Trp Arg Gly Cys Ile Pro Trp Pro Cys Pro Trp Arg Trp Arg
 305 310 315 320
 Trp Gly

(2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 528 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
 1 5 10 15
 His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
 20 25 30
 Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
 35 40 45
 Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
 50 55 60
 Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
 65 70 75 80
 Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala Leu Ile
 85 90 95

Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val Pro Gly
 100 105 110
 Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys Ala Glu Lys
 115 120 125
 Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu Tyr Gln
 130 135 140
 Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
 145 150 155 160
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
 165 170 175
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 180 185 190
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 195 200 205
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 210 215 220
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 225 230 235 240
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 245 250 255
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 260 265 270
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 275 280 285
 Lys Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 290 295 300
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 305 310 315 320
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 325 330 335
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 340 345 350
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 355 360 365
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 370 375 380
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 385 390 395 400
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 405 410 415
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 420 425 430

Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro
		435					440					445			
Val	Arg	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu
		450				455					460				
Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	His
465					470					475					480
Asp	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala
				485					490					495	
Arg	Leu	Ala	Lys	Glu	Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro
			500					505					510		
Leu	Glu	Val	Glu	Val	Gly	Ile	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Glu
		515					520					525			

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 315 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser	Gly
1				5					10					15	
Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly
			20					25					30		
His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr
		35				40						45			
Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu
	50					55					60				
Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp
65					70				75						80
Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	Lys	Ala
				85					90					95	
Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	Leu	Ile
			100					105					110		
Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val	Pro	Gly
		115					120					125			
Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	Lys	Ala	Glu	Lys
	130					135					140				
Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu	Tyr	Gln
145					150					155					160

Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr Leu Ile
 165 170 175
 Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp Gln Trp
 180 185 190
 Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu Pro Gly
 195 200 205
 Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp
 210 215 220
 Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala
 225 230 235 240
 Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu Ser Trp
 245 250 255
 Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp Phe Ala
 260 265 270
 Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu Glu Arg
 275 280 285
 Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro
 290 295 300
 Lys Ala Ala Leu Glu His His His His His His
 305 310 315

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600

TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GGCGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAACTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCC GCCAT	1140
AAAAA ACTCA TGTTC AAGAC AGAAG GGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCCTGT CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGCGC AGCTGTGGGT TGATTCCACA CCCCCGCCCC GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTTGTGA GGCCTGCCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGGCCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAGGGG AGCCTCACCA CGAGCTGCCC	900

CCAGGGAGCA CTAAGCGAGC ACTGCCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

ATGGAGGAGC CGCAGTCAGA TCCTAGCGTC GAGCCCCCTC TGAGTCAGGA AACATTTTCA	60
GACCTATGGA AACTACTTCC TGAAAACAAC GTTCTGTCCC CCTTGCCGTC CCAAGCAATG	120
GATGATTTGA TGCTGTCCCC GGACGATATT GAACAATGGT TCACTGAAGA CCCAGGTCCA	180
GATGAAGCTC CCAGAATGCC AGAGGCTGCT CCCCCCGTGG CCCCTGCACC AGCAGCTCCT	240
ACACCGGCGG CCCCTGCACC AGCCCCCTCC TGGCCCCGTG CATCTTCTGT CCCTTCCCAG	300
AAAACCTACC AGGGCAGCTA CGGTTTCCGT CTGGGCTTCT TGCATTCTGG GACAGCCAAG	360
TCTGTGACTT GCACGTACTC CCCTGCCCTC AACAAGATGT TTTGCCAACT GGCCAAGACC	420
TGCCCTGTGC AGCTGTGGGT TGATTCCACA CCCCCGCCG GCACCCGCGT CCGCGCCATG	480
GCCATCTACA AGCAGTCACA GCACATGACG GAGGTGTGTA GGCCTGCCC CCACCATGAG	540
CGCTGCTCAG ATAGCGATGG TCTGGCCCCCT CCTCAGCATC TTATCCGAGT GGAAGGAAAT	600
TTGCGTGTGG AGTATTTGGA TGACAGAAAC ACTTTTCGAC ATAGTGTGGT GGTGCCCTAT	660
GAGCCGCCTG AGGTTGGCTC TGACTGTACC ACCATCCACT ACAACTACAT GTGTAACAGT	720
TCCTGCATGG GCGGCATGAA CCGGAGACCC ATCCTCACCA TCATCACACT GGAAGACTCC	780
AGTGGTAATC TACTGGGACG GAACAGCTTT GAGGTGCGTG TTTGTGCCTG TCCTGGGAGA	840
GACCGGCGCA CAGAGGAAGA GAATCTCCGC AAGAAAAGGG AGCCTCACCA CGAGCTGCCC	900
CCAGGGAGCA CTAAGCGAGC ACTGCCCCAAC AACACCAGCT CCTCTCCCCA GCCAAAGAAG	960
AAACCACTGG ATGGAGAATA TTTCACCCTT CAGATCCGTG GCGGTGAGCG CTTCGAGATG	1020
TTCCGAGAGC TGAATGAGGC CTTGGAAGTC AAGGATGCCC AGGCTGGGAA GGAGCCAGGG	1080
GGGAGCAGGG CTCACTCCAG CCACCTGAAG TCCAAAAAGG GTCAGTCTAC CTCCCGCCAT	1140
AAAAAACTCA TGTTCAGAC AGAAGGGCCT GACTCAGACT GA	1182

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TCTGGGCTTC TTGCATTCTG 20

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GTTGGGCAGT GCTCGCTTAG 20

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTT CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGCG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GGCGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480

TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGCCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCCCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCGCAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300

CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCATGA ACCGGAGACC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGTCTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGTT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAGGATGGGA CTCCGGTTCA TG	22
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(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CATGAACCGG AGTCCCATCC TCAC

24

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GCACAAACAT GCACCTCAAA GCT

23

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CAGCTTTGAG GTGCATGTTT GT

22

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT

60

CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC

120

ACCCCCGCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC

180

GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC

240

TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGCGATGA ACCGGAGTCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCGT GTTTGTGCCT GTCCTGGGAG AGACCGGCGC ACAGAGGAAG AGAATCTCCG	540
CAAGAAAGGG GAGCCTCACC ACGAGCTGCC CCCAGGGAGC ACTAAGCGAG CACTGCCCAA	600
C	601

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GTTGGGCAGT GCTCGCTTAG TGCTCCCTGG GGGCAGCTCG TGGTGAGGCT CCCCTTTCTT	60
GCGGAGATTC TCTTCCTCTG TGCGCCGGTC TCTCCAGGA CAGGCACAAA CACGCACCTC	120
AAAGCTGTTC CGTCCCAGTA GATTACCACT GGAGTCTTCC AGTGTGATGA TGGTGAGGAT	180
GGGACTCCGG TTCATGCCGC CCATGCAGGA ACTGTTACAC ATGTAGTTGT AGTGGATGGT	240
GGTACAGTCA GAGCCAACCT CAGGCGGCTC ATAGGGCACC ACCACACTAT GTCGAAAAGT	300
GTTTCTGTCA TCCAAATACT CCACACGCAA ATTTCTTCC ACTCGGATAA GATGCTGAGG	360
AGGGGCCAGA CCATCGCTAT CTGAGCAGCG CTCATGGTGG GGGCAGCGCC TCACAACCTC	420
CGTCATGTGC TGTGACTGCT TGTAGATGGC CATGGCGCGG ACGCGGGTGC CGGGCGGGGG	480
TGTGGAATCA ACCACAGCT GCACAGGGCA GGTCTTGGCC AGTTGGCAAA ACATCTTGT	540
GAGGGCAGGG GAGTACGTGC AAGTCACAGA CTTGGCTGTC CCAGAATGCA AGAAGCCCAG	600
A	601

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 601 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCTGGGCTTC	TTGCATTCTG	GGACAGCCAA	GTCTGTGACT	TGCACGTACT	CCCCTGCCCT	60
CAACAAGATG	TTTTGCCAAC	TGGCCAAGAC	CTGCCCTGTG	CAGCTGTGGG	TTGATTCCAC	120
ACCCCCGCCC	GGCACCCGCG	TCCGCGCCAT	GGCCATCTAC	AAGCAGTCAC	AGCACATGAC	180
GGAGGTTGTG	AGGCGCTGCC	CCCACCATGA	GCGCTGCTCA	GATAGCGATG	GTCTGGCCCC	240
TCCTCAGCAT	CTTATCCGAG	TGGAAGGAAA	TTTGCGTGTG	GAGTATTTGG	ATGACAGAAA	300
CACTTTTTCGA	CATAGTGTGG	TGGTGCCCTA	TGAGCCGCCT	GAGGTTGGCT	CTGACTGTAC	360
CACCATCCAC	TACAACTACA	TGTGTAACAG	TTCTGTCATG	GGCGGCATGA	ACCGGAGGCC	420
CATCCTCACC	ATCATCACAC	TGGAAGACTC	CAGTGGTAAT	CTACTGGGAC	GGAACAGCTT	480
TGAGGTGCAT	GTTTGTGCCT	GTCCTGGGAG	AGACCGGCGC	ACAGAGGAAG	AGAATCTCCG	540
CAAGAAAGGG	GAGCCTCACC	ACGAGCTGCC	CCCAGGGAGC	ACTAAGCGAG	CACTGCCCAA	600
C						601

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GTTGGGCAGT	GCTCGCTTAG	TGCTCCCTGG	GGGCAGCTCG	TGGTGAGGCT	CCCCTTTCTT	60
GCGGAGATTC	TCTTCCTCTG	TGCGCCGGTC	TCTCCCAGGA	CAGGCACAAA	CATGCACCTC	120
AAAGCTGTTC	CGTCCCAGTA	GATTACCACT	GGAGTCTTCC	AGTGTGATGA	TGGTGAGGAT	180
GGGCCTCCGG	TTCATGCCGC	CCATGCAGGA	ACTGTTACAC	ATGTAGTTGT	AGTGGATGGT	240
GGTACAGTCA	GAGCCAACCT	CAGGCGGCTC	ATAGGGCACC	ACCACACTAT	GTCGAAAAGT	300
GTTTCTGTCA	TCCAAATACT	CCACACGCAA	ATTTCTTCC	ACTCGGATAA	GATGCTGAGG	360
AGGGGCCAGA	CCATCGCTAT	CTGAGCAGCG	CTCATGGTGG	GGGCAGCGCC	TCACAACCTC	420
CGTCATGTGC	TGTGACTGCT	TGTAGATGGC	CATGGCGCGG	ACGCGGGTGC	CGGGCGGGGG	480
TGTGGAATCA	ACCCACAGCT	GCACAGGGCA	GGTCTTGGCC	AGTTGGCAAA	ACATCTTGTT	540
GAGGGCAGGG	GAGTACGTGC	AAGTCACAGA	CTTGGCTGTC	CCAGAATGCA	AGAAGCCCAG	600
A						601

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCTGCATG GCGGCATGA ACCGGAGTCC	420
CATCCTC	427

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATGAACCGG AGTCCCATCC TCACCATCAT CACACTGGAA GACTCCAGTG GTAATCTACT	60
GGGACGGAAC AGCTTTGAGG TGC GTGTTT TGCCTGTCCT GGGAGAGACC GGCGCACAGA	120
GGAAGAGAAT CTCCGCAAGA AAGGGGAGCC TCACCACGAG CTGCCCCCAG GGAGCACTAA	180
GCGAGCACTG CCAAC	196

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 498 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TCTGGGCTTC TTGCATTCTG GGACAGCCAA GTCTGTGACT TGCACGTACT CCCCTGCCCT	60
CAACAAGATG TTTTGCCAAC TGGCCAAGAC CTGCCCTGTG CAGCTGTGGG TTGATTCCAC	120
ACCCCCGCCC GGCACCCGCG TCCGCGCCAT GGCCATCTAC AAGCAGTCAC AGCACATGAC	180
GGAGGTTGTG AGGCGCTGCC CCCACCATGA GCGCTGCTCA GATAGCGATG GTCTGGCCCC	240
TCCTCAGCAT CTTATCCGAG TGGAAGGAAA TTTGCGTGTG GAGTATTTGG ATGACAGAAA	300
CACTTTTCGA CATAGTGTGG TGGTGCCCTA TGAGCCGCCT GAGGTTGGCT CTGACTGTAC	360
CACCATCCAC TACAACTACA TGTGTAACAG TTCCTGCATG GCGGGCATGA ACCGGAGGCC	420
CATCCTCACC ATCATCACAC TGGAAGACTC CAGTGGTAAT CTACTGGGAC GGAACAGCTT	480
TGAGGTGCAT GTTTGTGC	498

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

CAGCTTTGAG GTGCATGTTT GTGCCTGTCC TGGGAGAGAC CGGCGCACAG AGGAAGAGAA	60
TCTCCGCAAG AAAGGGGAGC CTCACCACGA GCTGCCCCCA GGGAGCACTA AGCGAGCACT	120
GCCCAAC	127

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GGTTTTTCTT TGAGGTTTAG	20
-----------------------	----

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
GCGACACTCC ACCATAGAT 19

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:
CTGTCTTCAC GCAGAAAGC 19

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:
GCACGGTCTA CGAGACCTC 19

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:
GATCTACTAG TCATATGGAT 20

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:
TCGGTACCCG GGGATCCGAT 20

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATAAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGTGTGG GTCGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCCTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

CTGTCTTCAC GCAGAAAGCG TCTGGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGACTGTC TTCACGCAGA	120
AAGCGTCTAG CCATGGCGTT AGTATGAGTG TCGTGCAGCC TCCAGGACCC CCCCTCCCGG	180
GAGAGCCATA GTGGTCTGCG GAACCGGTGA GTACACCGGA ATTGCCAGGA CGACCGGGTC	240
CTTTCTTGGA TCAACCGCT CAATGCCTGG AGATTTGGGC GTGCCCCCGC AAGACTGCTA	300
GCCGAGTAGT GTTGGGTCGC GAAAGGCCTT GTGGTACTGC CTGATAGGGT GCTTGCGAGT	360
GCCCCGGGAG GTCTCGTAGA CCGTGC	386

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GTCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC TTGGATCAAC CCGCTCAATG CCTGGAGATT TGGGCGTGCC	180
CCCGCGAGAC TGCTAGCCGA GTAGTGTGG GTGCGGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTG CAGCCTCCAG	60
GACCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CAGGACGACC GGGTCCTTTC GTGGATGTAA CCCGCTCAAT GCCTGGAGAT TTGGGCGTGCC	180
CCCCGCAAGA CTGCTAGCCG AGTAGTGTGG GGTGCGGAAA GGCCTTGTGG TACTGCCTGA	240
TAGGGTGCTT GCGAGTGCCC CGGGAGGTCT CGTAGACCGT GC	282

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

CTGTCTTCAC GCAGAAAGCG TCTAGCCATG GCGTTAGTAT GAGTGTCGTA CAGCCTCCAG	60
GCCCCCCCCT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATTGC	120
CGGGAAGACT GGGTCCTTTC TTGGATAAAC CCACTCTATG CCCGGCCATT TGGGCGTGCC	180
CCCGCAAGAC TGCTAGCCGA GTAGCGTTGG GTTGCGAAAG GCCTTGTGGT ACTGCCTGAT	240
AGGGTGCTTG CGAGTACCCC GGGAGGTCTC GTAGACCGTG C	281

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
CTGTCTTCAC GCAGAAAGCG CCTAGCCATG GCGTTAGTAC GAGTGTCGTG CAGCCTCCAG      60
GACCCCCCTT CCCGGGAGAG CCATAGTGGT CTGCGGAACC GGTGAGTACA CCGGAATCGC      120
TGGGGTGACC GGGTCCTTTC TTGGAGCAAC CCGCTCAATA CCCAGAAATT TGGGCGTGCC      180
CCCGCGAGAT CACTAGCCGA GTAGTGTGGT GTCGCGAAAG GCCTTGTTGGT ACTGCCTGAT      240
AGGGTGCTTG CGAGTGCCCC GGGAGGTCTC GTAGACCGTG C                          281
```

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAGGCACCC TATCAGGCAG TACCACAAGG      60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG      120
GCATTGAGCG GGTTCATCCA AGAAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC      180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT      240
CATACTAACG CCATGGCCAG ACGCTTCTTG CGTGAAGACA G                          281
```

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTGTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTCGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTGTATCCA AGAAAGGACC CGGTCGTCCT GGCAATTCCG GTGTACTCAC	180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGA CCTGGAGGCT GCACGACACT	240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G	281

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG	60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATCTCCAG	120
GCATTGAGCG GGTACATCC ACGAAAGGAC CCGGTCGTCC TGGCAATTCC GGTGTACTCA	180
CCGGTTCCGC AGACCACTAT GGCTCTCCCG GGAGGGGGGG TCCTGGAGGC TGCACGACAC	240
TCATACTAAC GCCATGGCTA GACGCTTTCT GCGTGAAGAC AG	282

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
GCACGGTCTA CGAGACCTCC CGGGGTACTC GCAAGCACCC TATCAGGCAG TACCACAAGG      60
CCTTTTCGCAA CCCAACGCTA CTCGGCTAGC AGTCTTGCGG GGGCACGCCC AAATGGCCGG      120
GCATAGAGTG GGTTTATCCA AGAAAGGACC CAGTCTTCCC GGCAATTCCG GTGTACTCAC      180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGG CCTGGAGGCT GTACGACACT      240
CATACTAACG CCATGGCTAG ACGCTTTCTG CGTGAAGACA G                          281
```

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
GCACGGTCTA CGAGACCTCC CGGGGCACTC GCAAGCACCC TATCAGGCAG TACCACAAGG      60
CCTTTTCGCGA CCCAACACTA CTCGGCTAGT GATCTCGCGG GGGCACGCCC AAATTTCTGG      120
GTATTGAGCG GGTTGCTCCA AGAAAGGACC CGGTCACCCC AGCGATTCCG GTGTACTCAC      180
CGGTTCCGCA GACCACTATG GCTCTCCCGG GAGGGGGGGT CCTGGAGGCT GCACGACACT      240
CGTACTAACG CCATGGCTAG GCGCTTTCTG CGTGAAGACA G                          281
```

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
ATCAACATCC GGCCGGTGGT      20
```

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GGGGCCTCGC TACGGACCAG

20

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCG GGGTTGACCC ACAAGCGCCG ACTGTCGGCG	120
CTGGGGCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GCGGTTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCTG GGGTTGACCT ACAAGCGCCG ACTGTTCGGCG	120
CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ATCAACATCC GGCCGGTGGT CGCCGCGATC AAGGAGTTCT TCGGCACCAG CCAGCTGAGC	60
CAATTCATGG ACCAGAACAA CCCGCTGTCTG GGGTTGACCC ACAAGCGCCG ACTGTTGGCG	120
CTGGGGCCCCG GCGGTCTGTC ACGTGAGCGT GCCGGGCTGG AGGTCCGCGA CGTGCACCCG	180
TCGCACTACG GCCGGATGTG CCCGATCGAA ACCCCTGAGG GGCCCAACAT CGGTCTGATC	240
GGCTCGCTGT CGGTGTACGC GCGGGTCAAC CCGTTCGGGT TCATCGAAAC GCCGTACCGC	300
AAGGTGGTCG ACGGCGTGGT TAGCGACGAG ATCGTGTACC TGACCGCCGA CGAGGAGGAC	360
CGCCACGTGG TGGCACAGGC CAATTCGCCG ATCGATGCGG ACGGTCGCTT CGTCGAGCCG	420
CGCGTGCTGG TCCGCCGCAA GGCGGGCGAG GTGGAGTACG TGCCCTCGTC TGAGGTGGAC	480
TACATGGACG TCTCGCCCCG CCAGATGGTG TCGGTGGCCA CCGCGATGAT TCCCTTCCTG	540
GAGCACGACG ACGCCAACCG TGCCCTCATG GGGGCAAACA TGCAGCGCCA GGCGGTGCCG	600
CTGGTCCGTA GCGAGGCCCC	620

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT GGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCGGC ACGCTCACGT	480

GACAGACCGC CGGGCCCCAG CGCCGACAGT CGGCGCTTGT AGGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GGGGCCTCGC TACGGACCAG CGGCACCGCC TGGCGCTGCA TGTTTGCCCC CATGAGGGCA	60
CGGTTGGCGT CGTCGTGCTC CAGGAAGGGA ATCATCGCGG TGGCCACCGA CACCATCTGG	120
CGGGGCGAGA CGTCCATGTA GTCCACCTCA GACGAGGGCA CGTACTCCAC CTCGCCCCGC	180
TTGCGGCGGA CCAGCACGCG CGGCTCGACG AAGCGACCGT CCGCATCGAT CGGCGAATTG	240
GCCTGTGCCA CCACGTGGCG GTCCTCCTCG TCGGCGGTCA GGTACACGAT CTCGTCGCTA	300
ACCACGCCGT CGACCACCTT GCGGTACGGC GTTTCGATGA ACCCGAACGG GTTGACCCGC	360
GCGTACACCG ACAGCGAGCC GATCAGACCG ATGTTGGGCC CCTCAGGGGT TTCGATCGGG	420
CACATCCGGC CGTAGTGCGA CGGGTGACG TCGCGGACCT CCAGCCCCGC ACGCTCACGT	480
GACAGACCGC CGGGCCCCAG CGCCAACAGT CGGCGCTTGT GGTCAACCC CGACAGCGGG	540
TTGTTCTGGT CCATGAATTG GCTCAGCTGG CTGGTGCCGA AGAACTCCTT GATCGCGGCG	600
ACCACCGGCC GGATGTTGAT	620

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

AGCTCGTATG GCACCGGAAC	20
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(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

TTGACCTCCC ACCCGACTTG

20

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300

GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCGGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA GCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GGCGGCGTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

AGCTCGTATG GCACCGGAAC CGGTAAGGAC GCGATCACCA CCGGCATCGA GGTCGTATGG	60
ACGAACACCC CGACGAAATG GGACAACAGT TTCCTCGAGA TCCTGTACGG CTACGAGTGG	120
GAGCTGACGA AGAGCCCTGC TGGCGCTTGG CAATACACCG CCAAGGACGG CGCCGGTGCC	180
GGCACCATCC CGGACCCGTT CGGCGGGCCA GGGCGCTCCC CGACGATGCT GGCCACTGAC	240
CTCTCGCTGC GGGTGGATCC GATCTATGAG CGGATCACGC GTCGCTGGCT GGAACACCCC	300
GAGGAATTGG CCGACGAGTT CGCCAAGGCC TGGTACAAGC TGATCCACCG AGACATGGGT	360
CCCGTTGCGA GATACCTTGG GCCGCTGGTC CCCAAGCAGA CCCTGCTGTG GCAGGATCCG	420
GTCCCTGCGG TCAGCCACGA CCTCGTCGGC GAAGCCGAGA TTGCCAGCCT TAAGAGCCAG	480
ATCCTGGCAT CGGGATTGAC TGTCTCACAG CTAGTTTCGA CCGCATGGGC GCGGCGCTCG	540
TCGTTCCGTG GTAGCGACAA GCGCGGCGGC GCCAACGGTG GTCGCATCCG CCTGCAGCCA	600
CAAGTCGGGT GGGAGGTCAA	620

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 620 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCTGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCCCGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCTTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTCTGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```
TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC      60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA      120
GTCAATCCCG ATGCCCCGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG      180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC      240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG      300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC      360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG      420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CCGTGTATTG CCAAGCGCCA      480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC      540
CATTTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGG TGGTGATCGC GTCCTTACCG      600
GTTCCGGTGC CATACGAGCT                                     620
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(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```
TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC      60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA      120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG      180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC      240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG      300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC      360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG      420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CCGTGTATTG CCAAGCGCCA      480
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GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 620 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

TTGACCTCCC ACCCGACTTG TGGCTGCAGG CGGATGCGAC CACCGTTGGC GCCGCCGCGC	60
TTGTCGCTAC CACGGAACGA CGACGCCGCC GCCCATGCGG TCGAAACTAG CTGTGAGACA	120
GTCAATCCCG ATGCCAGGAT CTGGCTCTTA AGGCTGGCAA TCTCGGCTTC GCCGACGAGG	180
TCGTGGCTGA CCGCAGGGAC CGGATCCTGC CACAGCAGGG TCTGCTTGGG GACCAGCGGC	240
CCAAGGTATC TCGCAACGGG ACCCATGTCT CGGTGGATCA GCTTGTACCA GGCCTTGGCG	300
AACTCGTCGG CCAATTCCTC GGGGTGTTCC AGCCAGCGAC GCGTGATCCG CTCATAGATC	360
GGATCCACCC GCAGCGAGAG GTCAGTGGCC AGCATCGTCG GGGAGCGCCC TGGCCCGCCG	420
AACGGGTCCG GGATGGTGCC GGCACCGGCG CCGTCCTTGG CGGTGTATTG CCAAGCGCCA	480
GCAGGGCTCT TCGTCAGCTC CCACTCGTAG CCGTACAGGA TCTCGAGGAA ACTGTTGTCC	540
CATTTTCGTCG GGGTGTTCGT CCATACGACC TCGATGCCGC TGGTGATCGC GTCCTTACCG	600
GTTCCGGTGC CATAACGAGCT	620

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGAGTTTGAT CCTGGCTCAG	20
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(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GGCGGACGGG TGAGTAA 17

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

CTGCTGCCTC CCGTAGGAGT 20

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ATGACGTCAA GTCATCATGG CCCTTACGA 29

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GTACAAGGCC CGGGAACGTA TTCACCG 27

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GCAACGAGCG CAACCC 16

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ATGACGTCAA GTCATCATGG CCCTTA

26

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

AAATTGAAGA GTTTGATCAT GGCTCAGATT GAACGCTGGC GGCAGGCCTA ACACATGCAA	60
GTCGAACGGT AACAGGAAGA AGCTTGCTTC TTTGCTGACG AGTGGCGGAC GGGTGAGTAA	120
TGTCTGGGAA ACTGCCTGAT GGAGGGGGAT AACTACTGGA AACGGTAGCT AATACCGCAT	180
AACGTCGCAA GACCAAAGAG GGGGACCTTC GGGCCTCTTG CCATCGGATG TGCCCAGATG	240
GGATTAGCTA GTAGGTGGGG TAACGGCTCA CCTAGGCGAC GATCCCTAGC TGGTCTGAGA	300
GGATGACCAG CCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTGG	360
GGAATATTGC ACAATGGGCG CAAGCCTGAT GCAGCCATGC CGCGTGTATG AAGAAGGCCT	420
TCGGGTTGTA AAGTACTTTC AGCGGGGAGG AAGGGAGTAA AGTTAATACC TTTGCTCATT	480
GACGTTACCC GCAGAAGAAG CACCGGCTAA CTCCGTGCCA GCAGCCGCGG TAATACGGAG	540
GGTGCAAGCG TTAATCGGAA TTAAGTGGGCG TAAAGCGCAC GCAGGCGGTT TGTTAAGTCA	600
GATGTGAAAT CCCCAGGCTC AACCTGGGAA CTGCATCTGA TACTGGCAAG CTTGAGTCTC	660
GTAGAGGGGG GTAGAATTCC AGGTGTAGCG GTGAAATGCG TAGAGATCTG GAGGAATACC	720
GGTGGCGAAG GCGGCCCCCT GGACGAAGAC TGACGCTCAG GTGCCAAAGC GTGGGGAGCA	780
AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT GTCGACTTGG AGGTTGTGCC	840
CTTGAGGCGT GGCTTCCGGA GCTAACGCGT TAAGTCGACC GCCTGGGGAG TACGGCCGCA	900
AGGTTAAAAC TCAAATGAAT TGACGGGGGC CCGCACAAAGC GGTGGAGCAT GTGGTTTAAT	960
TCGATGCAAC GCGAAGAACC TTACCTGGTC TTGACATCCA CGGAAGTTTT CAGAGATGAG	1020
AATGTGCCTT CGGGAACCGT GAGACAGGTG CTGCATGGCT GTCGTCAGCT CGTGTTGTGA	1080

AATGTTGGGT TAAGTCCCGC AACGAGCGCA ACCCTTATCC TTTGTTGCCA GCGGTCCGGC	1140
CGGGAAGTCA AAGGAGACTG CCAGTGATAA ACTGGAGGAA GGTGGGGATG ACGTCAAGTC	1200
ATCATGGCCC TTACGACCAG GGCTACACAC GTGCTACAAT GGCGCATACA AAGAGAAGCG	1260
ACCTCGCGAG AGCAAGCGGA CCTCATAAAG TGCGTCGTAG TCCGGATTGG AGTCTGCAAC	1320
TCGACTCCAT GAAGTCGGAA TCGCTAGTAA TCGTGGATCA GAATGCCACG GTGAATACGT	1380
TCCCGGGCCT TGTACACACC GCCCGTCACA CCATGGGAGT GGGTTGCAAA AGAAGTAGGT	1440
AGCTTAACCT TCGGGAGGGC GCTTACCACT TTGTGATTCA TGACTGGGGT GAAGTCGTAA	1500
CAAGGTAACC GTAGGGGAAC CTGCGGTTGG ATCACCTCCT TA	1542

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

TTTTTATGGA GAGTTTGATC CTGGCTCAGA GTGAACGCTG GCGGCGTGCC TAATACATGC	60
AAGTCGAACG ATGAAGCTTC TAGCTTGCTA GAAGTGATT AGTGGCGCAC GGGTGAGTAA	120
GGTATAGTTA ATCTGCCCTA CACAAGAGGA CAACAGTTGG AAACGACTGC TAATACTCTA	180
TACTCCTGCT TAACACAAGT TGAGTAGGGA AAGTTTTTCG GTGTAGGATG AGACTATATA	240
GTATCAGCTA GTTGGTAAGG TAATGGCTTA CCAAGGCTAT GACGCTTAAC TGGTCTGAGA	300
GGATGATCAG TCACACTGGA ACTGAGACAC GGTCCAGACT CCTACGGGAG GCAGCAGTAG	360
GGAATATTGC GCAATGGGGG AAACCCTGAC GCAGCAACGC CGCGTGGAGG ATGACACTTT	420
TCGGAGCGTA AACTCCTTTT CTTAGGGAAG AATTCTGACG GTACCTAAGG AATAAGCACC	480
GGCTAACTCC GTGCCAGCAG CCGCGGTAAT ACGGAGGGTG CAAGCGTTAC TCGGAATCAC	540
TGGGCGTAAA GGGCGCGTAG GCGGATTATC AAGTCTCTTG TGAAATCTAA TGGCTTAACC	600
ATTAACTGC TTGGGAAACT GATAGTCTAG AGTGAGGGAG AGGCAGATGG AATTGGTGGT	660
GTAGGGGTAA AATCCGTAGA TATCACCAG AATACCCATT GCGAAGGCCA TCTGCTGGAA	720
CTCAACTGAC GCTAAGGCGC GAAAGCGTGG GGAGCAAACA GGATTAGATA CCCTGGTAGT	780
CCACGCCCTA AACGATGTAC ACTAGTTGTT GGGGTGCTAG TCATCTCAGT AATGCAGCTA	840
ACGCATTAAG TGTACCGCCT GGGGAGTACG GTCGCAAGAT TAAAACTCAA AGGAATAGAC	900
GGGGACCCGC ACAAGCGGTG GAGCATGTGG TTTAATTCTGA AGATACGCGA AGAACCTTAC	960
CTGGGCTTGA TATCCTAAGA ACCTTTTAGA GATAAGAGGG TGCTAGCTTG CTAGAACTTA	1020

GAGACAGGTG CTGCACGGCT GTCGTCAGCT CGTGTCGTGA GATGTTGGGT TAAGTCCCGC	1080
AACGAGCGCA ACCCACGTAT TTAGTTGCTA ACGGTTCCGGC CGAGCACTCT AAATAGACTG	1140
CCTTCGTAAG GAGGAGGAAG GTGTGGACGA CGTCAAGTCA TCATGGCCCT TATGCCCAGG	1200
GCGACACACG TGCTACAATG GCATATAGAA TGAGACGCAA TACCGCGAGG TGGAGCAAAT	1260
CTATAAAATA TGTCCCAGTT CGGATTGTTC TCTGCAACTC GAGAGCATGA AGCCGGAATC	1320
GCTAGTAATC GTAGATCAGC CATGCTACGG TGAATACGTT CCCGGGTCTT GTACTCACCG	1380
CCCGTCACAC CATGGGAGTT GATTTCACTC GAAGCCGGAA TACTAAACTA GTTACCGTCC	1440
ACAGTGGAAT CAGCGACTGG GGTGAAGTCG TAACAAGGTA ACCGTAGGAG AACCTGCGGT	1500
TGGATCACCT CCT	1513

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1555 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

TTTTATGGAG AGTTTGATCC TGGCTCAGGA TGAACGCTGG CGGCGTGCCT AATACATGCA	60
AGTCGAGCGA ACGGACGAGA AGCTTGCTTC TCTGATGTTA GCGGCGGACG GGTGAGTAAC	120
ACGTGGATAA CCTACCTATA AGACTGGGAT AACTTCGGGA AACCGGAGCT AATACCGGAT	180
AATATTTTGA ACCGCATGGT TCAAAAGTGA AAGACGGTCT TGCTGTCACT TATAGATGGA	240
TCCGCGCTGC ATTAGCTAGT TGGTAAGGTA ACGGCTTACC AAGGCAACGA TACGTAGCCG	300
ACCTGAGAGG GTGATCGGCC AACTGGAAC TGAGACACGG TCCAGACTCC TACGGGAGGC	360
AGCAGTAGGG AATCTTCCGC AATGGGCGAA AGCCTGACGG AGCAACGCCG CGTGAGTGAT	420
GAAGGTCTTC GGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG	480
CACATCTTGA CGGTACCTAA TCAGAAAGCC ACGGCTAACT ACGTGCCAGC AGCCGCGGTA	540
ATACGTAGGT GGCAAGCGTT ATCCGGAATT ATTGGGCGTA AAGCGCGCGT AGGCGGTTTT	600
TTAAGTCTGA TGTGAAAGCC CACGGCTCAA CCGTGAGGG TCATTGGAAA CTGGAAAAC	660
TGAGTGCAGA AGAGGAAAGT GGAATTCCAT GTGTAGCGGT GAAATGCGCA GAGATATGGA	720
GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC	780
GGGGATCAAA CAGGATTAGA TACCCTGGTA GTCCACGCCG TAAACGATGA GTGCTAAGTG	840
TTAGGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCTGGGGAGT	900
ACGACCGCAA GGTGAAACT CAAAGGAATT GACGGGGACC CGCACAAGCG GTGGAGCATG	960

TGGTTTAATT CGAAGCAACG CGAAGAACCT TACCAAATCT TGACATCCTT TGACAACTCT	1020
AGAGATAGAG CCTTCCCCTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC	1080
TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAAG CTTAGTTGCC	1140
ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGTGACAA ACCGGAGGAA GGTGGGGATG	1200
ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA	1260
AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT	1320
AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGTAGTAA TCGTAGATCA GCATGCTACG	1380
GTGAATACGT TCCCGGGTAT TGTACACACC GCCCGTCACA CCACGAGAGT TTGTAACACC	1440
CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG	1500
TGAAGTCGTA ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCT	1555

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: RNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAAUACUCAA GCUUGCAUGC CUGCAGGUCG ACUCUAGAGG AUCCCC	46
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(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

TTGACAATTA ATCATCGGCT CGTATAATGT GTGGAATTGT GAGCGGATAA CAATTTTACA	60
CAGGAAACAG CGATGAATTC GAGCTCGGTA CCCGGGGATC CTCTAGAGTC GACCTGCAGG	120
CATGCAAGCT TGGCACTGGC C	141

(2) INFORMATION FOR SEQ ID NO:163:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

AGATCTCGAT CCCGCGAAAT TAATACGACT CACTATAGGG AGACCACAAC GGTTTCCCTC	60
TAGAAATAAT TTTGTTTAAC TTTAAGAAGG AGATATACAT ATGGCTAGCA TGACTGGTGG	120
ACAGCAAATG GGTCGGATCC GGCT	144

(2) INFORMATION FOR SEQ ID NO:164:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAATACGACT CACTATAGGG AGACCGGAAT TCGAATCCG TGTATTCTAT AGTGTCACCT	60
AAATCGAATT C	71

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

CGCCAGGGTT TTCCAGTCA CGACGTTGTA AAACGACGGC CAGTGAATTG TAATACGACT	60
CACTATAGGG CGAATTCGAG CTCGGTACCC GGGGATCCTC TAGAGTCGAC CTGCAGGCAT	120
GCAAGCTTGA GTATTCTATA GTGTCACCTA AATAGCTTGG CGTAATCATG GTCATAGCTG	180
TTTCTGTGT GAAATTGTTA TCCGCTCACA ATTCCACACA ACATACGA	228